

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 16:32:15 ; Search time 160 Seconds
(without alignments)
2210.669 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRRIGALLLLPLAAVE.....ILNSIQVMRAQMNIQSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5181	99.9	1055	3 AAB19591	Aab19591 Human CAS
2	5181	99.9	1055	6 ABU07847	Abu07847 Human eph
3	5181	99.9	1055	8 ADL61215	Adl61215 Human pro
4	5177.5	99.8	987	3 AAB19590	Aab19590 Human CAS
5	5171.5	99.7	987	7 ADN39875	Adn39875 Cancer/an
6	5130	98.9	994	2 AAW26366	Aaw26366 Mouse Nuk
7	5130	98.9	994	4 AAU01907	Aau01907 Murine ne
8	5126	98.8	994	2 AAR87018	Aar87018 Receptor
9	5093	98.2	970	2 AAR85089	Aar85089 EPH-like
10	4993.5	96.3	995	2 AAR75712	Aar75712 Eph-relat
11	4971.5	95.8	1011	2 AAR75709	Aar75709 Eph-relat
12	4936	95.1	969	8 ADO28627	Ado28627 Human EPH
13	3934.5	75.8	984	7 ADE63400	Ad63400 Rat Prote
14	3934.5	75.8	984	7 ADE83380	Ad83380 Rat Prote
15	3926.5	75.7	984	2 AAR44513	Aar44513 elk. 6/19
16	3924	75.6	984	7 ADE83382	Ad83382 Human Pro
17	3924	75.6	984	7 ADF09563	Adf09563 Human Eph
18	3715.5	71.6	951	2 AAR75704	Aar75704 Eph-relat
19	3670.5	70.7	998	7 ADN39865	Adn39865 Cancer/an
20	3669	70.7	973	2 AAR75708	Aar75708 Eph-relat
21	3662.5	70.6	988	2 AAR75710	Aar75710 Eph-relat
22	3661.5	70.6	998	6 ABU07849	Abu07849 Human eph
23	3661.5	70.6	998	7 ADE38343	Ad38343 Human pro
24	3661.5	70.6	998	7 ADD93259	Ad93259 CCMP-1.1
25	3661.5	70.6	998	8 ADQ20030	Adq20030 Human sof

AB111903 Human pro
Aar51899 Human emb
Aar75843 Protein p
Aar75844 Protein p
Adj71136 Human hea
Aar75707 EPH-relat
Aar5090 EPH-like
Aar52826 Human rec
Aar5091 EPH-like
Aar46395 Human pro
Aar7780 Human sof
Aar5689 Novel hum
Aar52931 Novel hum
Aar44241 Tyrosine
Aar5936 Protein t
Aar61868 Prostata
Aar31683 Human 141
Aar52827 Human EHK
Aar5092 EPH-like
Aar3421 Mouse dev
Aar29342 Human nov
Aar08665 Amino aci
Aar3583 Human rec
Aar5273 Prostata
Aar48947 Human pro
Aar3284 Cancer/an
Aar08666 A human E
Aar57491 Human EPH
Aar52825 Chicken r
Aar75711 EPH-relat
Aar48945 Rat Prote
Aar31466 HEK polyp
Aar57136 Mouse isc
Aar5930 Protein t
Aar89263 Human non
Aar06335 Full leng
Aar1304 Receptor-
Aar94652 Receptor
Aar67398 Amino aci
Aar34081 Human Pro
Aar32033 Human Kin
Aar01372 Human PRO
Aar43801 Human sec
Aar43569 Human sec
Aar01244 Human PRO
Aar01128 Human sec
Aar43685 Human sec
Aar06947 Human PRO
Aar08435 Novel hum
Aar99728 Human PRO
Aar87011 Human PRO
Aar66166 Human sec
Aar99844 Human PRO
Aar99499 Novel hum
Aar66050 Human sec
Aar23448 Human tra
Aar26141 Human PRO
Aar04968 Human PRO
Aar1274 Human PRO
Aar8205 Human PRO
Aar5500 Human PRO
Aar06430 Human PRO
Aar38205 Human PRO
Aar8321 Human PRO
Aar89321 Human sec
Aar12509 Human KSE
Aar99457 Human sec
Aar06550 Human PRO
Aar06550 Human PRO
Aar82502 Human PRO
Aar51755 Human sec
Aar51871 Human sec

Age37729 Human sec
Ade37613 Human sec

99 2835 54.6 1036 8 ADE37729
100 2835 54.6 1036 8 ADE37613

ALIGNMENTS

RESULT 1
AAB19591
ID AAB19591 standard; protein; 1055 AA.

XX AC AAB19591;
DT 22-JAN-2001 (first entry)
XX DE Human CASB616.

CASB616; EPHB2; ERK; EPH3; EPH3; EPH3; DRT; HEK5; EPHB2v;
receptor protein tyrosine kinase; human; antigen; colon cancer;
ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WO200053216-A2.

XX PD 14-SEP-2000.

XX PF 28-FEB-2000; 2000WO-EP001587.

XX PR 05-MAR-1999; 99GB-00005124.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX FI Vinals Y De Bassolac;

XX DR WPI; 2000-587384/55.

XX DR N-PSDB; AAA88549.

XX PT Vaccine composition for treating ovarian and colon cancer, comprises
CASB616 polypeptides, polynucleotides or antigen presenting cells
expressing the polypeptides.

XX PS Claim 1; Page 42; 57pp; English.

CC The present sequence is that of human CASB616, a member of the EPH and
CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616
CC polypeptides and polynucleotides are important immunogens for specific
CC prophylactic or therapeutic immunization against tumours, especially
CC colon cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal cells
CC and can thus be targeted by antigen-specific immune mechanisms leading to
CC destruction of the tumour cells. They can also be used to diagnose the
CC occurrence of tumour cells. Their inappropriate expression can also cause
CC an induction of autoimmune responses, which can be corrected through
CC vaccination using the CASB616 polypeptides or polynucleotides

XX SQ Sequence 1055 AA;

Query Match 99.9%; Score 5181; DB 3; Length 1055;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRLGALLLLPLLAARETLLMDSTTATLAEGLWVHPSPGWEVSGYDNNMTITYQ 60

DB 1 MALRLGALLLLPLLAARETLLMDSTTATLAEGLWVHPSPGWEVSGYDNNMTITYQ 60

QY 61 VCNVFESSQNNWLRTKFIIRRGARHRIHVEMKFSVRDCSSIPSPGCKETFNLYYEADF 120

DB 61 VCNVFESSQNNWLRTKFIIRRGARHRIHVEMKFSVRDCSSIPSPGCKETFNLYYEADF 120

QY 121 DSATKTFPNWENPWVKVDTTAADESFQVDLGGVRVWKINTEVRSFGPVSRSFYLAFO 180

DB 121 DSATKTFPNWENPWVKVDTTAADESFQVDLGGVRVWKINTEVRSFGPVSRSFYLAFO 180

QY 181 YGCMSLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

DB 181 YGCMSLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTCVRCGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300

DB 241 CNGDGEWLVPIGRCMCKAGFEAVENGTCVRCGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300

QY 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNI 360

DB 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNI 360

QY 361 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 420

DB 361 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 420

QY 421 SPOFASVNTTNOAAPSASVIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYKEKSE 480

DB 421 SPOFASVNTTNOAAPSASVIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYKEKSE 480

QY 481 YNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEK 540

DB 481 YNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIOEK 540

QY 541 LPLIIGSSAAGLVFLIAVVVIAIVCNRRGERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600

DB 541 LPLIIGSSAAGLVFLIAVVVIAIVCNRRGERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600

QY 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660

DB 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660

QY 661 EKORRDFLSEASIMGQFDHPNVTHLEGVTKSTPVMIIITEFMENGLSDSFLRNDGQFTV 720

DB 661 EKORRDFLSEASIMGQFDHPNVTHLEGVTKSTPVMIIITEFMENGLSDSFLRNDGQFTV 720

QY 721 IQLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780

DB 721 IQLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780

QY 781 TSALGKGIPIRTAPEAIQYRKFTSASDVMSYGIWVMEVMSYGERPYWMTNQDVINAIE 840

DB 781 TSALGKGIPIRTAPEAIQYRKFTSASDVMSYGIWVMEVMSYGERPYWMTNQDVINAIE 840

QY 841 QDYRLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGI 900

DB 841 QDYRLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGI 900

QY 901 NLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDDVVSQMMEDILRLGVTL 960

DB 901 NLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDDVVSQMMEDILRLGVTL 960

QY 961 AGHOKKILNSIQWRAQMNIQSV 985

DB 961 AGHOKKILNSIQWRAQMNIQSV 985

RESULT 2
ABU07847
ID ABU07847 standard; protein; 1055 AA.

XX AC ABU07847;

DT 10-MAY-2003 (first entry)

DE Human ephrin receptor ligand EphB2.

KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;

KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;

KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;

KW cell migration disorder; cell proliferation disorder; neovascularisation;

ischaemia; infarction; tissue graft; transplant; human; ephrin receptor ligand; tie receptor tyrosine kinase; EphB2.

Homo sapiens.

W02003004529-A2.

16-JAN-2003.

02-JUL-2002; 2002WO-IB002524.

02-JUL-2001; 2001US-0302960P.

(LICN) LICENTIA LTD.

Alitalo K, Kubo H;

WPI; 2003-210341/20.

N-PSDB; ABX12548.

Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative modulator.

Disclosure; Page 128-132; 199pp; English.

The invention describes a method of identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. The method comprises contacting a Tie receptor composition with an Ephrin composition in the presence and in the absence of a putative modulator compound, and detecting the binding between the Tie receptor and the Ephrin in the presence and in the absence of the putative modulator. The method is useful for identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. Modulators identified from the method are useful in modulating angiogenic processes, including lymphangiogenesis, for treating diseases associated with aberrant Ephrin-Tie biology, aberrant growth, migration or proliferation of cells that express a Tie receptor, or for promoting growth of vessel or neovascularisation (e.g. ischaemic tissue, an infarction, a new or chronic compound, or a tissue graft or transplant). This is the amino acid sequence of human EphB2, a member of the Ephrin-B subclass of ligands that are bound to the membrane via a transmembrane domain and short cytoplasmic tail and function as Ephrin receptor ligands

Sequence 1055 AA;

Query Match	99.9%;	Score 5181;	DB 6;	Length 1055;					
Best Local Similarity	99.9%;	Pred. No. 0;							
Matches 984;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;					
QY	1	MALRRLGAALLLLP	LAARETLMDS	TATAELGMMVHP	PPSGWEVSGYDENMNTIRTYQ	60			
DB	1	MALRRLGAALLLLP	LAARETLMDS	TATAELGMMVHP	PPSGWEVSGYDENMNTIRTYQ	60			
QY	61	VCNVFESSQNNLRTK	FIRRGGAHRIH	VEKFSVRDC	SSIPSPGSKCTFNLYYYEADF	120			
DB	61	VCNVFESSQNNLRTK	FIRRGGAHRIH	VEKFSVRDC	SSIPSPGSKCTFNLYYYEADF	120			
QY	121	DSATKTPNNMENPW	KVDITIADES	FSQVDLGRV	NKINTEVRSF	GPVRSRGPFLAFQD	180		
DB	121	DSATKTPNNMENPW	KVDITIADES	FSQVDLGRV	NKINTEVRSF	GPVRSRGPFLAFQD	180		
QY	181	YGGCMSLIAVRV	FRKCPRIION	CAIFQETLS	GAESTSLVA	ARGSCIANAEVDVPIKLY	240		
DB	181	YGGCMSLIAVRV	FRKCPRIION	CAIFQETLS	GAESTSLVA	ARGSCIANAEVDVPIKLY	240		
QY	241	CNGDGEWLVP	IGRCMC	KAGFEAV	ENGTVCR	GCPSGTFKANQ	GDCACTHCPINRSTTSEGA	300	
DB	241	CNGDGEWLVP	IGRCMC	KAGFEAV	ENGTVCR	GCPSGTFKANQ	GDCACTHCPINRSTTSEGA	300	
QY	301	TNCVCRNGYYRAD	LDPLDM	CTTIPSA	QAVISSV	NETSLMLEW	TPPRD	SGGRDLVYNI	360

301	TNCVCRNGYYRAD	LDPLDM	CTTIPSA	QAVISSV	NETSLMLEWTPPRD	SGGRDLVYNI	360																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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421	SPOFASVNTTNOAAPS	AVSIMHQVSR	TVDSITLSWSQ	POPNGVILDYELQYKEKELSE	480																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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481	YNATAIKSP	TNTVTVOGLKAG	AIYVQVRART	VAGYGRYSKMY	FQMTAEYQTSIQEK	540																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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601	TYEDPNEA	VREFAKEID	ISCVKIEQ	VIGAGEF	GEVCSGHLKLPGR	EIFVAIKTLKSGYT	660																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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661	EKORRDF	LSSEAS	IMGQFDH	PNVIHL	EGVVTKSTPM	LIITEFMENGSLDSFLRQNDGQFTV	720																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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721	IQLVGLM	RGIAAG	KYLAD	MN	VYVHRDLAARN	ILVNSLVCKVSD	FGLSRFLEDDTSDPT	780																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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841	QDYRL	PPMD	CP	SAL	HQ	LM	DC	WK	OR	NHR	PKFG	QIVNTLD	KMIR	PNSL	KAM	AP	LS	SGI	900																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
841	QDYRL	PPMD	CP	SAL	HQ	LM	DC	WK	OR	NHR	PKFG	QIVNTLD	KMIR	PNSL	KAM	AP	LS	SGI	900																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
901	NLP	LLD	RT	IP	DY	TS	FN	T	DE	W	LE	AI	K	M	G	Q	Y	K	S	F	A	N	A	G	F	T	S	F	D	V	V	S	Q	M	M	E	D	I	L	R	L	G	V	T	L	960																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
901	NLP	LLD	RT	IP	DY	TS	FN	T	DE	W	LE	AI	K	M	G	Q	Y	K	S	F	A	N	A	G	F	T	S	F	D	V	V	S	Q	M	M	E	D	I	L	R	L	G	V	T	L	960																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
961	AGH	QK	I	L	N	S	I	Q	V	M	R	A	Q	M	N	I	Q	S	V	E	985																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									

RESULT 3

ADL61215

ID ADL61215 standard; protein; 1055 AA.

XX AC ADL61215;

XX AC ADL61215;

DT 03-JUN-2004 (first entry)

XX Human protein tyrosine kinase biomarker EphB2 protein.

DE predictor set; protein tyrosine kinase; cytostatic; antiangiogenic;

XX vasotrophic; vulnery; pharmacogenomic; drug sensitivity; breast cancer;

KW hypervascular disease; angiogenesis; wound healing scar; human;

KW biomarker; EphB2.

XX Homo sapiens.

OS Homo sapiens.

XX WO2004020583-A2.

PN 11-MAR-2004.

XX 26-AUG-2003; 2003WO-US026491.

XX 27-AUG-2002; 2002US-0406385P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PA

XX Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY;
PI Shaw P;
XX WPI; 2004-239171/22.
DR N-PSDB; ADL61078.
XX
PT New predictor sets with a plurality of polynucleotides and/or
PT polypeptides whose expression pattern predicts cell response to a
PT compound that modulates protein tyrosine kinase activity, useful in
PT treating breast cancer.
XX
XX Claim 9; SEQ ID NO 139; 649pp; English.
XX
XX The invention relates to a novel predictor set comprising a plurality of
XX polynucleotides and/or polypeptides whose expression pattern is
XX predictive of the response of cells to treatment with a compound that
XX modulates protein tyrosine kinase activity or members of the protein
XX tyrosine kinase pathway. The molecules of the invention demonstrate
XX cytosolic, antiangiogenic, vasotropic and vulnerary activities and may
XX be useful in the field of pharmacogenomics, in particular for determining
XX drug sensitivity and in treating breast cancer, hypervascular diseases, of
XX angiogenesis and scars in wound healing. The current sequence is that of
XX a human protein tyrosine kinase biomarker protein of the invention.
XX
XX Sequence 1055 AA;
SQ

Query Match 99.9%; Score 5181; DB 8; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRLGAALLLLPAAVEETLMDSTTATAELGMMVHPSPSGEVSQYDENMTIRTYQ 60
Db 1 MALRLGAALLLLPAAVEETLMDSTTATAELGMMVHPSPSGEVSQYDENMTIRTYQ 60
Qy 61 VCNVFESSQNNWLRTKFIIRRGARHIVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120
Db 61 VCNVFESSQNNWLRTKFIIRRGARHIVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120
Qy 121 DSATKTPNNMENPWKVDTTAADESFSQVLDGRVMKINTEVRSFGVPSRSGYLAPOD 180
Db 121 DSATKTPNNMENPWKVDTTAADESFSQVLDGRVMKINTEVRSFGVPSRSGYLAPOD 180
Qy 181 YGGCMLIAVFRYKCPRIIIONGAIQFTLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db 181 YGGCMLIAVFRYKCPRIIIONGAIQFTLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Qy 241 CNGDGEMLVPIGRMCCKAGFAVENGTVCRCGPGSGTFRKANQGDCACTHCPINSRTTSEGA 300
Db 241 CNGDGEMLVPIGRMCCKAGFAVENGTVCRCGPGSGTFRKANQGDCACTHCPINSRTTSEGA 300
Qy 301 TNCVCRNGYYRADLDPLDMPCTTIPSAQAVISSVNETSLMELWTPPRDSGREDLVYNI 360
Db 301 TNCVCRNGYYRADLDPLDMPCTTIPSAQAVISSVNETSLMELWTPPRDSGREDLVYNI 360
Qy 361 CKSCGSRGACTRCGDNVQAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDQSPF 420
Db 361 CKSCGSRGACTRCGDNVQAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDQSPF 420
Qy 421 SPQFASVNTTNOAPSASVIMHVSRTVDSITLSWSQPDQPNQVILDYELQYKEKELSE 480
Db 421 SPQFASVNTTNOAPSASVIMHVSRTVDSITLSWSQPDQPNQVILDYELQYKEKELSE 480
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Qy 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRGFERRADSEYTDKLOHTYSGHMTFGMKIYIDPF 600
Db 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRGFERRADSEYTDKLOHTYSGHMTFGMKIYIDPF 600
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660
Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660

Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660
Qy 661 EKORDFLSEASIMGOFDHPNVHLEGVVTKSTPMWITTEFMENGLSDSFLRQNDGQFTV 720
Db 661 EKORDFLSEASIMGOFDHPNVHLEGVVTKSTPMWITTEFMENGLSDSFLRQNDGQFTV 720
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSLVCKVSDFLSFLSDEDDTSDPTY 780
Db 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSLVCKVSDFLSFLSDEDDTSDPTY 780
Qy 781 TSALGKIPIRWTAPETAIQYRKFTSASDVWSVGIUWVEVMSYGERPYWMTQDVINAIE 840
Db 781 TSALGKIPIRWTAPETAIQYRKFTSASDVWSVGIUWVEVMSYGERPYWMTQDVINAIE 840
Qy 841 QYRLPPPMDCPSALHOLMLDCWQDRNHRPKFGQIVNTLDKWRNPNSLKAMAPLSSGI 900
Db 841 QYRLPPPMDCPSALHOLMLDCWQDRNHRPKFGQIVNTLDKWRNPNSLKAMAPLSSGI 900
Qy 901 NLPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGTSTFDVVSQMMEDILRIGVTL 960
Db 901 NLPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGTSTFDVVSQMMEDILRIGVTL 960
Qy 961 AGHQKILNSIQVMRAQMNQIOSVE 985
Db 961 AGHQKILNSIQVMRAQMNQIOSVE 985

RESULT 4
AAB19590
ID AAB19590 standard; protein; 987 AA.
XX
AC AAB19590;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CASB616.
XX
KW CASB616; EPB2; ERK; EPB3; EPHT3; DRT; HEK5; EPB2v;
KW receptor protein tyrosine kinase; human; antigen; colon cancer;
KW ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 568..569
FT FT /note= "an additional Arg residue decodes from the
FT CASB616 nucleotide sequence given in the specification
FT (see AAA88548), but is not given in the CASB616 amino
FT acid sequence in the specification"
FT FT Misc-difference 956
FT FT /note= "encoded by GTT"
XX
XX WO200053216-A2.
XX
XX 14-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-EP001587.
XX
XX 05-MAR-1999; 99GB-00005124.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Vinals Y De BassolsC;
XX
XX WPI; 2000-587384/55.
XX
XX N-PSDB; AAA88548.
XX
XX Vaccine composition for treating ovarian and colon cancer, comprises
XX CASB616 polypeptides, polynucleotides or antigen presenting cells
XX expressing the polypeptides.
XX
XX Claim 1; Page 41; 57pp; English.

CC The present sequence is that of human CASB616, a member of the EPH and
CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616
CC polypeptides and polynucleotides are important immunogens for specific
CC prophylactic or therapeutic immunization against tumours, especially
CC colon cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal cells
CC and can thus be targeted by antigen-specific immune mechanisms leading to
CC destruction of the tumour cells. They can also be used to diagnose the
CC occurrence of tumour cells. Their inappropriate expression can also cause
CC an induction of autoimmune responses, which can be corrected through
CC vaccination using the CASB616 polypeptides or polynucleotides
XX
SQ Sequence 987 AA;

Query Match 99.8%; Score 5177.5; DB 3; Length 987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 986; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MALRRGAALLLLPAAVEETLMDSTTATAELGMMVHPSPGSGVEVGYDENMTIRTYQ 60
Db 1 MALRRGAALLLLPAAVEETLMDSTTATAELGMMVHPSPGSGVEVGYDENMTIRTYQ 60

Qy 61 VCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPVCSCKETFNLYYEADF 120
Db 61 VCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPVCSCKETFNLYYEADF 120

Qy 121 DSATKTPFNMMENPWKVDVTTAADESPQDLGRVWKINTEVSPGVSRSGLYLAPOD 180
Db 121 DSATKTPFNMMENPWKVDVTTAADESPQDLGRVWKINTEVSPGVSRSGLYLAPOD 180

Qy 181 YGGCMSLIAVVFYRKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db 181 YGGCMSLIAVVFYRKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

Qy 241 CNGDEMLVPIGRWCCKAGFAVNGTVCRGCPGTFKANGQDEACTHCPINSTRTSEGA 300
Db 241 CNGDEMLVPIGRWCCKAGFAVNGTVCRGCPGTFKANGQDEACTHCPINSTRTSEGA 300

Qy 301 TNCVCRNGYRADLDPLDMPCTTIPSAQVAVISSVNETSLMWTTPRDSGREDLYVNI 360
Db 301 TNCVCRNGYRADLDPLDMPCTTIPSAQVAVISSVNETSLMWTTPRDSGREDLYVNI 360

Qy 361 CKSCGSGRAGTACGDNVQAPQGLTEPRIVISDLAHTQYTFEIQAVNGVTDOSPF 420
Db 361 CKSCGSGRAGTACGDNVQAPQGLTEPRIVISDLAHTQYTFEIQAVNGVTDOSPF 420

Qy 421 SPQFASVNTTNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSE 480
Db 421 SPQFASVNTTNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSE 480

Qy 481 YNATAIKSPNTVTVOGLKAGAVVFOVARTVAGYGRYSKMYFQMTWAEYQTSIOEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAVVFOVARTVAGYGRYSKMYFQMTWAEYQTSIOEK 540

Qy 541 LPLIIGSSAAGLVFLIAVWVIAVCN-RRGERADSEYTKLQHYTSGHMTPGMKIYIDP 599
Db 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRGERADSEYTKLQHYTSGHMTPGMKIYIDP 600

Qy 600 PTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFEGVCSGHLKLPKREIFVAIKLKSQY 659
Db 601 PTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFEGVCSGHLKLPKREIFVAIKLKSQY 660

Qy 660 TEKORRDLFSLASIMGQPDHNVTHLEGVVTKSPVMIITFEFMENGLSDSLRQNDQFT 719
Db 661 TEKORRDLFSLASIMGQPDHNVTHLEGVVTKSPVMIITFEFMENGLSDSLRQNDQFT 720

Qy 720 VIQLVGLMRGIAAGWKYLDMMVYHRLAARNILVNSNLVCKVSDPGLSFLRQNDQFT 779
Db 721 VIQLVGLMRGIAAGWKYLDMMVYHRLAARNILVNSNLVCKVSDPGLSFLRQNDQFT 780

Qy 780 YTSALGGKIPIRWTAPEAIQYRKFTSADSWSYGIVVMVMSYGERPYWDMTNOVDINAI 839
Db YTSALGGKIPIRWTAPEAIQYRKFTSADSWSYGIVVMVMSYGERPYWDMTNOVDINAI 839

Db 781 YTSALGGKIPIRWTAPEAIQYRKFTSADSWSYGIVVMVMSYGERPYWDMTNOVDINAI 840
Qy 840 EQDYRLPPPPMDCPSALHQLMDCWQKDNHRPKFGQIVVTLTKMIRPNPSLKAWAPLSSG 899
Db 841 EQDYRLPPPPMDCPSALHQLMDCWQKDNHRPKFGQIVVTLTKMIRPNPSLKAWAPLSSG 900
Qy 900 INLPDLLDRTTIPDYTSFNTVDEWLEAIKVGQYKESFANAGTSPFDVVSQMMEDILRLGVT 959
Db 901 INLPDLLDRTTIPDYTSFNTVDEWLEAIKVGQYKESFANAGTSPFDVVSQMMEDILRLGVT 960
Qy 960 LAGHOKKILNSIQVMRAQMNQIQSV 986
Db 961 LAGHOKKILNSIQVMRAQMNQIQSV 987

RESULT 5
ADN39875
ID ADN39875 standard; protein; 987 AA.
XX
AC ADN39875;
XX AC
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C245.
XX Human; differential expression; cancer; angiogenic disorder;
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
XX inflammatory disease; autoimmune disease;
XX retinal neovascularisation syndrome; scarring; uterine fibroid;
XX detection; diagnosis; prognosis; drug screening; drug targeting;
XX wound healing; contraception; cytostatic; cardiant; immunomodulatory;
XX vulnery; gene therapy; vaccine.
XX Homo sapiens.
XX WO2003042661-A2.
XX 22-MAY-2003.
XX 13-NOV-2002; 2002WO-US036810.
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-0355250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-0368809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-0372246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
XX N-PSDB; ADN39658.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO C245; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 987 AA;

Query Match 99.7%; Score 5171.5; DB 7; Length 987;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 984; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 MALRRLLGAALLLLPDLAABETLMDSTTATAELGMMVHPSPGWEVSGYDENMTTIRTYQ 60
DB 1 MALRRLLGAALLLLPDLAABETLMDSTTATAELGMMVHPSPGWEVSGYDENMTTIRTYQ 60

QY 61 VCNVFESSQNNWLRTKFIERRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120
DB 61 VCNVFESSQNNWLRTKFIERRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120

QY 121 DSATKTFPNMENPWKVDITTADESQVDLGRVVKINTEVRSFQVPSRSGFYLAQD 180
DB 121 DSATKTFPNMENPWKVDITTADESQVDLGRVVKINTEVRSFQVPSRSGFYLAQD 180

QY 181 YGGCMSLIIVAVFRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
DB 181 YGGCMSLIIVAVFRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

QY 241 CNGDGEWLVPITGRCMWKAGFEAVENGTVCRGCPSTFKANQGDACHTCPINRTTSEGA 300
DB 241 CNGDGEWLVPITGRCMWKAGFEAVENGTVCRGCPSTFKANQGDACHTCPINRTTSEGA 300

QY 301 TNCVCRNGYRADLDPLDMPCTTIPSAQVAVISSVNETSLMEWTPRDSGGREDLYVNI 360
DB 301 TNCVCRNGYRADLDPLDMPCTTIPSAQVAVISSVNETSLMEWTPRDSGGREDLYVNI 360

QY 361 CKSCGSGRGACTRCGDNVQVAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPF 420
DB 361 CKSCGSGRGACTRCGDNVQVAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPF 420

QY 421 SPQFASVNIITNOAAPSASVIMHQVSRVDSITLSWSQPPQNGVILDYELQYKEKELSE 480
DB 421 SPQFASVNIITNOAAPSASVIMHQVSRVDSITLSWSQPPQNGVILDYELQYKEKELSE 480

QY 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
DB 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540

QY 541 LPLIIGSSAAGLVFLIAVWVIAVCN-RRGPERADSEYTDKLOHYTSGHMTPGMKIYIDP 599
DB 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRRGERADSEYTDKLOHYTSGHMTPGMKIYIDP 600

QY 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAFGEVCSGHLKLPKREIFVAILKLSGY 659
DB 601 FTYEDPNEAVREFAKEIDISCVKIEQVIGAFGEVCSGHLKLPKREIFVAILKLSGY 660

QY 660 TEKORRFLSEASIMGQFDHNVHLEGVVTKSPVMIITEFMENGSLDSFLRQNDGQFT 719
DB 661 TEKORRFLSEASIMGQFDHNVHLEGVVTKSPVMIITEFMENGSLDSFLRQNDGQFT 720

QY 720 VIQVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 779
DB 721 VIQVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 780

QY 780 YTSALGKGKIPIRWTAPEAIQYRFTSASDVWSYGIWVWEVWSYGERPYWDMTQDVINAI 839
DB 781 YTSALGKGKIPIRWTAPEAIQYRFTSASDVWSYGIWVWEVWSYGERPYWDMTQDVINAI 840

QY 840 EODYRLPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWIENPNSLKAWAPLSSG 899
DB 841 EODYRLPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWIENPNSLKAWAPLSSG 900

QY 900 INLPLDRTIPDYSFNTVDLEALIKWQYKESFANAGFTSPDVVVSQMMEDILRLGVT 959
DB 901 INLPLDRTIPDYSFNTVDLEALIKWQYKESFANAGFTSPDVVVSQMMEDILRLGVT 960

QY 960 LAGHQKKILNSIQVMRAQMNQIOSVEV 986
DB 961 LAGHQKKILNSIQVMRAQMNQIOSVEV 987

RESULT 6
AAW26366
ID AAW26366 standard; protein; 994 AA.
XX
AC AAW26366;
XX
DT 02-DEC-1997 (first entry)
XX
DE Mouse Nuk tyrosine kinase.
XX
KW Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;
KW axonogenesis; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; multiple sclerosis;
KW amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;
KW ischaemia; stroke.
XX
OS Mus musculus.
XX
PH Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Sig_peptide 27..994
FT Domain /label= Mat_protein 27..548
FT Region /label= Extracellular_domain 330..420
FT Region /note= FNIII
FT Region /note= "fibronectin type III repeat" 444..534
FT Domain /label= FNIII
FT Domain /note= "fibronectin type III repeat" 549..574
FT Domain /label= Transmembrane_domain 575..994
FT Region /label= Cytoplasmic_domain 623..888
FT Region /label= Tyrosine-kinase_region
XX WO9714966-A1.
XX
XX 24-APR-1997.
XX
XX 10-OCT-1996; 96WO-CA000679.
XX
XX 13-OCT-1995; 95US-0005518P.
XX
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
XX Pawson A, Henkemeyer M;
XX WPI; 1997-245245/22.
XX N-PSDB; AAT84528.
DR

XX Activation of ligand regulatory pathways by Eph subfamily receptor
PT tyrosine kinases - for stimulating or inhibiting axonogenesis, useful for
PT treatment of e.g. neurodegenerative diseases such as Alzheimer's or
PT Parkinson's diseases.
XX Disclosure; Fig 3; 55pp; English.
XX Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase
CC that is essential for formation of the medial tract of the anterior
CC commissure of the brain, and which appears to play a role in the
CC formation of the habenular interpeduncular tract. Its amino acid sequence
CC was deduced from cDNA clones (see AAR84528) isolated from an embryo cDNA
CC library. The extracellular domain of Nuk was shown to be sufficient for
CC formation of the medial tract. Eph subfamily receptor tyrosine kinases
CC (e.g. the Nuk extracellular domain) can be used in claimed methods to:
CC activate a ligand regulatory pathway in a cell; identify substances able
CC to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to
CC affect neuronal development or regeneration, especially the stimulation
CC or inhibition of axonogenesis, in a mammal. Activation of the ligand
CC regulatory pathway results in downstream activation of a series of
CC regulatory pathways in cells that control gene expression, cell division,
CC cytoskeletal architecture, cell metabolism, cell migration and cell-cell
CC interactions. Substances which activate the ligand regulatory pathway may
CC be used for stimulating or inhibiting neuronal development regeneration
CC and axonal migration associated with neurodegenerative disease e.g.
CC Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis,
CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's
CC disease, peripheral nerve damage, trauma and ischaemia resulting from
CC stroke
XX Sequence 994 AA;

Query Match 98.9%; Score 5130; DB 2; Length 994;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAAVEETLMDSTTATAELAGMNVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ 69
DB 18 LLLPLLAAVEETLMDSTTATAELAGMNVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ 77
QY 70 NNWLRTFPIRRGARRHIVEMKFSVRDCSSIPSPGCKETFNLYYEADPDSATKTFPN 129
DB 78 NNWLRTFPIRRGARRHIVEMKFSVRDCSSIPSPGCKETFNLYYEADPDLATKTFPN 137
QY 130 WMENPWKVDITIADESFSQVDLGRVYKINTEVRSFGPVSRSFGYLAFOYGGCMSLIA 189
DB 138 WMENPWKVDITIADESFSQVDLGRVYKINTEVRSFGPVSRSFGYLAFOYGGCMSLIA 197
QY 190 VRVPRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGSEWL 249
DB 198 VRVPRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGSEWL 257
QY 250 PIGRCMKAGFEAVENGTVCRGCPSPGTFKANQGDGEACTHCPINSRTTSEGATNCVCNRY 309
DB 258 PIGRCMKAGFEAVENGTVCRGCPSPGTFKANQGDGEACTHCPINSRTTSEGATNCVCNRY 317
QY 310 YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR 369
DB 318 YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR 377
QY 370 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFASVNI 429
DB 378 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFASVNI 437
QY 430 TTNOAPSASVIMHQVSRVDSITLSWQDPQPNVILDYELQYKEKSEYNATAIKSP 489
DB 438 TTNOAPSASVIMHQVSRVDSITLSWQDPQPNVILDYELQYKEKSEYNATAIKSP 497
QY 490 TINTVVOGLKAGALYVFOVARTVAGYGRYSGKMYFQMTAEAYQTSIQSKLPLIGSSA 549
DB 498 TINTVVOGLKAGALYVFOVARTVAGYGRYSGKMYFQMTAEAYQTSIQSKLPLIGSSA 557

QY 550 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTVEDNEAV 609
DB 558 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTVEDNEAV 617
QY 610 REFKAIDIDSCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 669
DB 618 REFKAIDIDSCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 677
QY 670 EASIMQFQDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQLVGMRLG 729
DB 678 EASIMQFQDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQLVGMRLG 737
QY 730 IAAGMKYLAADNMVYVHRDLAARNILVNSNLVCKVSDFGSLRFLDEDDTSDPYTSALGQKIP 789
DB 738 IAAGMKYLAADNMVYVHRDLAARNILVNSNLVCKVSDFGSLRFLDEDDTSDPYTSALGQKIP 797
QY 790 IRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTNQDVINAIEQDYRLPPPM 849
DB 798 IRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTNQDVINAIEQDYRLPPPM 857
QY 850 DCPALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTTI 909
DB 858 DCPALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTTI 917
QY 910 PDYTSNTVDWELEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTLAGHQKILN 969
DB 918 PDYTSNTVDWELEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTLAGHQKILN 977
QY 970 SIQVMAQNMNIQSV 986
DB 978 SIQVMAQNMNIQSV 994
RESULT 7
AAU01907
ID AAU01907 standard; protein; 994 AA.
XX
XX AAU01907;
XX AC AC
XX XX
DT 29-AUG-2001 (first entry)
XX
DE Murine neural kinase (Nuk) polypeptide.
XX
XX Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;
KW nerve fibre; cell-cell interaction; axonogenesis; neuronal development;
KW regeneration; neurodegenerative disorder; Alzheimer's disease; ischaemia;
KW Parkinson's disease; Huntington's disease; demyelinating disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;
KW Wernicke's disease; nutritional polyneuropathy; multistem degeneration;
KW progressive supranuclear palsy; Shy Drager's syndrome; mouse;
KW olivoponto cerebellar atrophy; peripheral nerve damage.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..26
FT /note= "Signal peptide"
FT Domain 26..548
FT /note= "Extracellular domain, preferably residues 26-544"
FT Protein 27..994
FT /note= "Mature murine neural kinase"
FT Domain 52..119
FT /note= "Ig-like domain"
FT Region 239..268
FT /note= "Ig-like Nuk repeat"
FT Region 330..420
FT /note= "Fibronectin type III repeat"
FT Region 444..534
FT /note= "Fibronectin type III repeat"
FT Domain 549..574
FT /note= "Hydrophobic transmembrane domain"
FT Binding-site 600..618
FT /note= "SH2 domain binding site"

FT Region 601..994
 FT /note= "Carboxy terminal"
 FT Modified-site 604..613
 FT /note= "Phosphorylation site"
 FT Domain 623..888
 FT /note= "Catalytic tyrosine kinase domain"
 FT Binding-site 623..707
 FT /note= "ATP binding site"
 XX US6218356-B1.
 XX 17-APR-2001.
 XX 13-OCT-1995; 95US-00542635.
 XX 29-APR-1994; 94US-00235407.
 XX 28-APR-1995; 95WO-CA000254.
 XX (MOUN) MOUNT SINAI HOSPITAL CORP.
 XX Pawson A, Henkemeyer M, Letwin K;
 XX WPI; 2001-289845/30.
 XX N-PSDB; AAS03612.
 XX New composition comprising neural receptor tyrosine kinase protein useful
 XX for inhibiting or stimulating axonogenesis, neuronal development, or
 XX regeneration and axonal migration.
 XX Claim 1; Fig 2; 86pp; English.
 XX The sequence represents a mouse neural kinase (Nuk) polypeptide. The
 XX murine Nuk locus has been mapped to the distal end of chromosome four.
 XX The polypeptide is a novel receptor tyrosine kinase protein, and is found
 XX to be expressed at high levels within migrating axons and is associated
 XX with nerve fibres. It functions to regulate specific cell-cell
 XX interactions during early development of the nervous system and in
 XX axonogenesis. Substances which bind to the Nuk protein, particularly
 XX ligands, may be used for stimulating or inhibiting neuronal development,
 XX regeneration and axonal migration associated with neurodegenerative
 XX disorders and conditions involving trauma and injury to the nervous
 XX system. These disorders include Alzheimer's disease, Parkinson's disease,
 XX Huntington's disease, demyelinating diseases such as multiple sclerosis,
 XX amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's
 XX disease and nutritional polyneuropathy, progressive supranuclear palsy,
 XX Shy Drager's syndrome, multistep degeneration, olivoponto cerebellar
 XX atrophy, peripheral nerve damage, and ischaemia resulting from stroke.
 XX The proteins may be used to prepare antibodies having specificity for Nuk
 XX proteins, which can be used to diagnose or treat disorders of the nervous
 XX system. These proteins are also used for screening agonists or
 XX antagonists of the interactions of the Nuk proteins with binding
 XX molecules
 XX
 SQ Sequence 994 AA;
 Query Match 98.9%; Score 5130; DB 4; Length 994;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 10 LLLPLLAANVEETLMDSTTATAELGWNVHPSPGHEEVSVDENNNNTTIRTYQVCNVFESSQ 69
 DB 18 LLLPLLAANVEETLMDSTTATAELGWNVHPSPGHEEVSVDENNNNTTIRTYQVCNVFESSQ 77
 QY 70 NNWLRTKFIIRRRGAHRTHVEMKFSVRDCSSIPSPVPGSKCTFNLYYYEADFDATKTFPN 129
 DB 78 NNWLRTKFIIRRRGAHRTHVEMKFSVRDCSSIPSPVPGSKCTFNLYYYEADFDATKTFPN 137
 QY 130 WMENPWVKVDITAADESFSQVDLGGRVYMKINTEVRSFGPVSRSFGYLAFOYGGCMSLIA 189
 DB 138 WMENPWVKVDITAADESFSQVDLGGRVYMKINTEVRSFGPVSRSFGYLAFOYGGCMSLIA 197
 QY 190 VRVYRKCPIRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGBWLV 249

Db 198 VRVYRKCPIRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGBWLV 257
 QY 250 PIGRCMKAGFEAVENGTCVRCGPGSGTFKANOGEACTHCPINSRTTSEGATNCVCNGY 309
 Db 258 PIGRCMKAGFEAVENGTCVRCGPGSGTFKANOGEACTHCPINSRTTSEGATNCVCNGY 317
 QY 310 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369
 Db 318 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 377
 QY 370 GACTRCGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 429
 Db 378 GACTRCGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 437
 QY 430 TTNOAPSASVIMHOVSRTVDSITLSWSQDQNGVILDYELQYKEKSEYNATAIKSP 489
 Db 438 TTNOAPSASVIMHOVSRTVDSITLSWSQDQNGVILDYELQYKEKSEYNATAIKSP 497
 QY 490 TINTVTVOGLKAGAIYVQVRARTVAGYGRYSGRMVFQTMTEABYQTSIOEKLPIIIGSSA 549
 Db 498 TINTVTVOGLKAGAIYVQVRARTVAGYGRYSGRMVFQTMTEABYQTSIOEKLPIIIGSSA 557
 QY 550 AGLVFLIAVVIIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAV 609
 Db 558 AGLVFLIAVVIIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAV 617
 QY 610 REFAKEIDISCKIEQVIGAGEFGEVCSGHLKLPGRKEIFVATKTLKSGYTEKQRDFLS 669
 Db 618 REFAKEIDISCKIEQVIGAGEFGEVCSGHLKLPGRKEIFVATKTLKSGYTEKQRDFLS 677
 QY 670 EASIMGQFHPNVIHLEGVVTKSTPVMIITEFMENGLSDSLFRQNDGQFTVIOLVGMRLG 729
 Db 678 EASIMGQFHPNVIHLEGVVTKSTPVMIITEFMENGLSDSLFRQNDGQFTVIOLVGMRLG 737
 QY 730 IAAGMYLADNVVHRLDAAARNILVNSLVCKVDFGLSRFLBDDTSDPTTYSALGSKIP 789
 Db 738 IAAGMYLADNVVHRLDAAARNILVNSLVCKVDFGLSRFLBDDTSDPTTYSALGSKIP 797
 QY 790 IRTAPEAIQYRKFTSASDVWSYGIWVWEVMSYGERPYMDMTNQDVINAEQDYRLPPPM 849
 Db 798 IRTAPEAIQYRKFTSASDVWSYGIWVWEVMSYGERPYMDMTNQDVINAEQDYRLPPPM 857
 QY 850 DCPSSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNLSKAMAPLSSGINLPLDRTI 909
 Db 858 DCPSSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNLSKAMAPLSSGINLPLDRTI 917
 QY 910 PDYTSNTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHOKKILN 969
 Db 918 PDYTSNTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHOKKILN 977
 QY 970 SIQVMRAQNMNIOQSV 986
 Db 978 SIQVMRAQNMNIOQSV 994
 RESULT 8
 AAR87018
 ID AAR87018 standard; protein; 994 AA.
 XX AAR87018;
 XX 19-MAR-1996 (first entry)
 DT Receptor tyrosine kinase (neural kinase).
 XX Receptor tyrosine kinase; neural kinase; Nuk; axon; axonogenesis;
 XX nerve disorder.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide i..26
 FT /label= Sig_peptide

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FT Region 27. 548
FT /label= Extracellular_region
FT /note= "the extracellular region (amino acids 27-548)
FT includes an N-terminal Ig-like domain and an Ig-like Nuk
FT repeat"
FT 330..420
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 444..534
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 549..574
FT /label= Transmembrane_region
FT 575..994
FT /label= Cytoplasmic_region
FT 623..707
FT /label= Tyrosine-kinase_catalytic_domain
XX WO9530326-A1.
XX 09-NOV-1995.
XX 28-APR-1995; 95WO-CA000254.
XX 29-APR-1994; 94US-00235407.
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX Pawson A, Henkemeyer M, Letwin K;
XX WPI; 1995-393299/50.
XX N-PSDB; AAT07308.
XX
XX DNA encoding neural receptor tyrosine kinase - useful in gene therapy of
XX nerve disorders, and for diagnosis and identification of therapeutic
XX agents.
XX Claim 1; Page 70-74; 103pp; English.
XX
XX A novel receptor tyrosine kinase (AAR87018), designated neural kinase
XX (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obt'd from a mouse embryo
XX library. Nuk is expressed in migrating axons and is involved in cell-cell
XX interactions and axonogenesis in development of the nervous system. Nuk
XX or its fragments (pref. amino acids 26-548 or 601-994) are used to
XX identify (ant)agonists of the (activated) receptor tyrosine kinase as a
XX means of treating nerve disorders and damage, or to raise antibodies used
XX to monitor axon migration and nerve cell interactions
XX
XX Sequence 994 AA;
XX
XX Query Match 98.8%; Score 5126; DB 2; Length 994;
XX Best Local Similarity 99.4%; Pred. No. 0;
XX Matches 971; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX 10 LLLPLLAAVEETLMDSTTATAELGWMVHPSPGWEESVGYDENNNNTIRTYQVCNVESSQ 69
XX |
XX 18 LLLPLLAAVEETLMDSTTATAELGWMVHPSPGWEESVGYDENNNNTIRTYQVCNVESSQ 77
XX |
XX 70 NNMLRTKPIRRRGAHRTHVEMKFSVRDCSSITPSVPGSKETENLYYYEADFDSATKTFPN 129
XX |
XX 78 NNMLRTKPIRRRGAHRTHVEMKFSVRDCSSITPSVPGSKETENLYYYEADFDLATKTFPN 137
XX |
XX 130 WMENPWVKVDITIAADESFSQVDLGGRVWKINTEVRSFGPVSRSGFYLAFODYGCMSLIA 189
XX |
XX 138 WMENPWVKVDITIAADESFSQVDLGGRVWKINTEVRSFGPVSRNGFYLAFODYGCMSLIA 197
XX |
XX 190 VRVPYRKCPRIIQNGAIFQBTLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
XX |
XX 198 VRVPYRKCPRIIQNGAIFQBTLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257
XX |
XX 250 PIGRCMKAGFEAVENGTVCRCPSGTFKANOQDEACTHCPINSRTTSEGATNCVCNGY 309
XX |
XX 258 PIGRCMKAGFEAVENGTVCRCPSGTFKANOQDEACTHCPINSRTTSEGATNCVCNRNGY 317
XX |

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310 YRADLDPLDMPTTIPSAPOAVISSVNETSIMLEWTTPRDSGGREDLVYNIICKSCGSGR 369
318 YRADLDPLDMPTTIPSAPOAVISSVNETSIMLEWTTPRDSGGREDLVYNIICKSCGSGR 377
370 GACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTOQSPPOFASVNI 429
378 GACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTOQSPPOFASVNI 437
430 TTNOAPSASVIMHOVSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 489
438 TTNOAPSASVIMHOVSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 497
490 TINTVVOGLKAGAIYVQVRARTVAGYGRYSGRMVFTQMTAEAYQTSIQEKLPLIIGSSA 549
498 TINTVVOGLKAGAIYVQVRARTVAGYGRYSGRMVFTQMTAEAYQTSIQEKLPLIIGSSA 557
550 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAV 609
558 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAV 617
610 REFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYTEKORRDFLS 669
618 REFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYTEKORRDFLS 677
670 EASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLG 729
678 EASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLG 737
730 IAAGMKYLADNMVYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPYTTSALGKIP 789
738 IAAGMKYLADNMVYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPYTTSALGKIP 797
790 IRTAPEAIQYRKFTSASDVMSYGIWMVEVMSYGERPYDMTQDVINAIEQDYRLPPPM 849
798 IRTAPEAIQYRKFTSASDVMSYGIWMVEVMSYGERPYDMTQDVINAIEQDYRLPPPM 857
850 DCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIKRNPNLSLKAMAPLSSGINPLLDRTI 909
858 DCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIKRNPNLSLKAMAPLSSGINPLLDRTI 917
910 PDYTSNTVDWEUAEIATMGQYKESFANAGTSPDFVVSQMMMEDILRLGVTLAGHQKILN 969
918 PDYTSNTVDWEUAEIATMGQYKESFANAGTSPDFVVSQMMMEDILRLGVTLAGHQKILN 977
970 SIQVMEARQMNQIOSVEV 986
978 SIQVMEARQMNQIOSVEV 994

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RESULT 9
AAR85089
ID AAR85089 standard; protein; 970 AA.
XX
AC AAR85089;
XX
DT 16-APR-1996 (first entry)
XX
DE EPH-like receptor protein tyrosine kinase HEKS.
XX
KW EPH-like receptor protein tyrosine kinase; PTK; HEKS;
human eph-like kinase; therapy; diagnosis; vector; antibody.
OS Homo sapiens.
XX
PN WO9528484-A1.
XX
PD 26-OCT-1995.
XX
PF 14-APR-1995; 95WO-US004681.
XX
PR 15-APR-1994; 94US-00229509.
XX

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PA	(AMGE-) AMGEN INC.	615	EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM	674
XX				
PI	Fox GM, Welcher AA, Jing S;	599	EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM	658
XX				
DR	WPI; 1995-373799/48.	675	QGFDPHNVHLEGVVTKSTPVMIIIFEFMENGSLDSFLRNDGQFTVIQLVGMLRGAAGM	734
XX				
DR	N-PSDB; AAT02946.	659	GQFDHENVHLEGVVTKSTPVMIIIFEFMENGSLDSFLRNDGQFTVIQLVGMLRGAAGM	718
XX				
PT	New nucleic acid encoding Eph-like receptor tyrosine kinase(s) - and	735	KYLADNNVYHRLDAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA	794
XX				
PT	related vectors, host cells, proteins, antibodies etc., used	719	KYLADNNVYHRLDAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA	778
XX				
PT	diagnostically and therapeutically to modulate receptor activation or	795	PEAIQYRKFTSASDVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPMDCPSA	854
XX				
XX	prodn.	779	PEAIQYRKFTSASDVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPMDCPSA	838
XX				
PS	Claim 18; Page 46-49; 133pp; English.	855	LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS	914
XX				
XX	4 Novel human Eph-like receptor protein tyrosine kinases, HEK5, HEK7,	839	LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS	898
CC	HEK8 and HEK11 (AAR85089-92), respectively, were identified following			
CC	isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain	915	FNTVDEWLEAIKMGQYKESFANAGFTSFVDSVQMMEDILRLGVTLGHHQKILNSIQVM	974
CC	cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the			
CC	catalytic domain of chicken Eph-like receptors Cdk5, Cdk7 and Cdk8. HEK11	899	FNTVDEWLEAIKMGQYKESFANAGFTSFVDSVQMMEDILRLGVTLGHHQKILNSIQVM	958
CC	shows no homology to any known Eph-like receptor. Recombinant HEK			
CC	receptors (or their soluble extracellular domains) are produced by	975	RAQMNQIQSVEV 986	
CC	expression of encoding sequences in prokaryotic or eucaryotic host cells,			
CC	and are used to produce antibodies (utilised in diagnostic assays), or to	959	RAQMNQIQSVEV 970	
CC	identify and purify ligands for HEK receptors, or therapeutically to			
CC	modulate the activation of cell-associated receptors. Soluble HEK5			
CC	receptor may affect primarily brain and pancreatic cells			
XX				
XX	Sequence 970 AA;			
SQ				
Query Match 98.2%; Score 5093; DB 2; Length 970;				
Best Local Similarity 99.5%; Pred. No. 0;				
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;				
QY	15 LLAAVEITLMDSTTATAELGMMVPPSGMEVSGYDENMTIRTYQVCNVFESSQNWL 74			
DB	1 LLAAVEITLMDSTTATAELGMMVPPSGMEVSGYDENMTIRTYQVCNVFESSQNWL 60			
QY	75 TKFIRRGARHIVEMKFSVRDSCSIPSPGCKETFNLYYEADFDSATKTFPNWENP 134			
DB	61 TKFIRRGARHIVEMKFSVRDSCSIPSPGCKETFNLYYEADFDSATKTFPNWENP 120			
QY	135 WVKVDTTAADESFQVLDGRVMKINTEVRSFGVSRSGFYLAPODYGGCMSLIARVVFY 194			
DB	121 WVKVDTTAADESFQVLDGRVMKINTEVRSFGVSRSGFYLAPODYGGCMSLIARVVFY 180			
QY	195 RKPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 254			
DB	181 RKPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240			
QY	255 MCKAGFEAVENGTVCRGCPSTGTFKANQDEACTHCPINRSTTSEGATNCVCRNGYRADL 314			
DB	241 MCKAGFEAVENGTVCRGCPSTGTFKANQDEACTHCPINRSTTSEGATNCVCRNGYRADL 300			
QY	315 DPLDMPCTTIPSAQVAVISSVNETSLMWTTPRDSGREDLVNIIICKSGSGRGACTR 374			
DB	301 DPLDMPCTTIPSAQVAVISSVNETSLMWTTPRDSGREDLVNIIICKSGSGRGACTR 360			
QY	375 CGDNVQVAPROGLGTEPRYIISDLAHTQYFEIQAQVNGVTDQSPSPQFASVNIITNQ 434			
DB	361 CGDNVQVAPROGLGTEPRYIISDLAHTQYFEIQAQVNGVTDQSPSPQFASVNIITNQ 420			
QY	435 APSAVSMHVSRTVDSITLWSOPDPNGVILDYELQYVEKELSEYNATAIKSPNTVT 494			
DB	421 APSAVSMHVSRTVDSITLWSOPDPNGVILDYELQYVEKELSEYNATAIKSPNTVT 480			
QY	495 VQGLKAGAIYVQVARTVAGYGYSGKMPQNTWEAYQTSIQEKLPLIGSSAAGLVF 554			
DB	481 --GLKAGAIYVQVARTVAGYGYSGKMPQNTWEAYQTSIQEKLPLIGSSAAGLVF 538			
QY	555 LIAVWVIAVNCRRGFERADSEYTDKLOHTYSGHMTFCMKIYIDPFTYEDPNEAVREPAK 614			
DB	539 LIAVWVIAVNCRRGFERADSEYTDKLOHTYSGHMTFCMKIYIDPFTYEDPNEAVREPAK 598			
Query Match 96.3%; Score 4993.5; DB 2; Length 995;				
Best Local Similarity 95.8%; Pred. No. 0;				
QY	615 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM			
DB	599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM			
QY	675 QGFDPHNVHLEGVVTKSTPVMIIIFEFMENGSLDSFLRNDGQFTVIQLVGMLRGAAGM			
DB	659 GQFDHENVHLEGVVTKSTPVMIIIFEFMENGSLDSFLRNDGQFTVIQLVGMLRGAAGM			
QY	735 KYLADNNVYHRLDAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA			
DB	719 KYLADNNVYHRLDAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA			
QY	795 PEAIQYRKFTSASDVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPMDCPSA			
DB	779 PEAIQYRKFTSASDVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPMDCPSA			
QY	855 LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS			
DB	839 LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS			
QY	915 FNTVDEWLEAIKMGQYKESFANAGFTSFVDSVQMMEDILRLGVTLGHHQKILNSIQVM			
DB	899 FNTVDEWLEAIKMGQYKESFANAGFTSFVDSVQMMEDILRLGVTLGHHQKILNSIQVM			
QY	975 RAQMNQIQSVEV 986			
DB	959 RAQMNQIQSVEV 970			
RESULT 10				
AAR75712				
ID	AAR75712 standard; protein; 995 AA.			
XX				
AC	AAR75712;			
XX				
DT	25-MAR-2003 (revised)			
DT	11-NOV-1995 (first entry)			
XX				
DE	Eph-related PTK Cdk5.			
XX				
KW	Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis; prognosis.			
XX				
OS	Gallus sp.			
XX				
PN	WO9515375-A1.			
XX				
PD	08-JUN-1995.			
XX				
PF	07-SEP-1994; 94WO-US010140.			
XX				
PR	03-DEC-1993; 93US-00162809.			
XX				
PA	(LJOL-) LA JOLLA CANCER RES FOUND.			
XX				
PI	Pasquale EB, Sajjadi FG;			
XX				
DR	WPI; 1995-215256/28.			
XX				
DR	N-PSDB; AAO90660.			
XX				
PT	Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing			
XX				
PS	cancer.			
XX				
PS	Disclosure; Page 92-96; 129pp; English.			
XX				
CC	Probes derived from the Eph-related PTKs Cdk4 (AAQ90659) and Cdk5			
CC	(AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58, AAQ90661-			
CC	62) from chicken embryo and embryonic brain libraries. (Updated on 25-MAR			
CC	-2003 to correct PN field.)			
XX				
SQ	Sequence 995 AA;			

Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;			
Qy	10	LLLLPLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ	69
Db	18	LALLPLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ	77
Qy	70	NNMLRTKPIRRRGAAHRIHVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADFDSATKTFPN	129
Db	78	NNMLRTKPIRRRGAAHRIHVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADFDSATKTFPN	137
Qy	130	WMENPWKVDITIAADESFQVDLGGVRVMTNTEVRSPGVSRSFGFYLAFOYGGCMLIA	189
Db	138	WMENPWKVDITIAADESFQVDLGGVRVMTNTEVRSPGVSRSFGFYLAFOYGGCMLIA	197
Qy	190	VRVYRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV	249
Db	198	VRVYRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV	257
Qy	250	PIGRCKAGFEAVENGTCVRCGCPSTGTFKANOQDEACTHCPINSRTTSEGATNCVCENGY	309
Db	258	PIGRCKRPGYESVENGTVCRCGCPSTGTFKASQDEGCVHCPINSRTTSEGATNCVCENGY	317
Qy	310	YRADLPDLMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR	369
Db	318	YRADADPVDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR	377
Qy	370	GACTRCGDNVQAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI	429
Db	378	GACTRCGDNVQAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI	437
Qy	430	TTNQAPSAVSIMHOVSRTVDSITLSWSQDPQPNVILDYELQYKELSEYNATAIKSP	489
Db	438	TTNQAPSAVSIMHOVSRTVDSITLSWSQDPQPNVILDYELQYKELSELNSTAVKSP	497
Qy	490	TNTVTUOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEVQTSIQEKLPIIIGSSA	549
Db	498	TNTVTUOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEVQTSIQEKLPIIIGSSA	557
Qy	550	AGLVFLAVVIAIVCN-RRGFERADSEYTDKLOHTSGHMTGPKMIYIDPFTYEDNEA	608
Db	558	AGLVFLAVVIAIVCN-RRGFERADSEYTDKLOHTSGHMTGPKMIYIDPFTYEDNEA	617
Qy	609	VREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDFL	668
Db	618	VREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDFL	677
Qy	669	SEASIMQFDPHPNVIHLEGVVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVQLVGMRL	728
Db	678	SEASIMQFDPHPNVIHLEGVVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVQLVGMRL	737
Qy	729	GIAAGMKYLAADNVVHRDLAARNILVNSLVCKVSDFLGRFLBDDTSDPTYSALGCKI	788
Db	738	GIAAGMKYLAADNVVHRDLAARNILVNSLVCKVSDFLGRFLBDDTSDPTYSALGCKI	797
Qy	789	PIRWTAPEALQYRKFTSASDVMSYGIWVWVMSYGERPYMDMTNQDVINAIEQDYRLPPP	848
Db	798	PIRWTAPEALQYRKFTSASDVMSYGIWVWVMSYGERPYMDMTNQDVINAIEQDYRLPPP	857
Qy	849	MDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKQIRNPNSLKAMAPLSSGINPLLDRT	908
Db	858	MDCPNALHQLMDCQKDRNHRPKFGQIVNTLDKQIRNPNSLKAMAPLSSGINPLLDRT	917
Qy	909	IPDVTSTNTVDWELEAKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLACHOKKIL	968
Db	918	IPDVTSTNTVDWELEAKMGQYKESFASAGFTTIDVVSQMTVEDILRLGVTLACHOKKIL	977
Qy	969	NSIQVMAQNMNIQSVVEV 986	
Db	978	NSIQVMAQNMNIQSVVEV 995	

QY 430 TTNQAPSAVSIHQVSRITSLWSQDPQNGVILDYELQYERKELSEYNATAIKSP 489
DB 438 TTNQAPSAVSIHQVSRITSLWSQDPQNGVILDYELQYERKELSEYNATAIKSP 497
QY 490 TTTVQGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSA 549
DB 498 TTTVQGLKAGTIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSA 557
QY 550 AGLVFLAVVIAVCN- RGFERADSEYTDKLOHYSGH-----MTPG 592
DB 558 AGLVFLAVVIAVCN- RGFERADSEYTDKLOHYSGH-----MTPG 617
QY 593 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAI 652
DB 618 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAI 677
QY 653 KTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLR 712
DB 678 KTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLR 737
QY 713 QNDGQFTVIOVLGMLRGIAAGMKYLADMYVHRDLAARNILVNSLVCKVSDGLSRFLE 772
DB 738 QNDGQFTVIOVLGMLRGIAAGMKYLADMYVHRDLAARNILVNSLVCKVSDGLSRFLE 797
QY 773 DDTSDPTYSALGGKIPIRWTAPPAIQRKFTASDVMSYGVIMVWVMSYGERPYWDMTN 832
DB 798 DDTSDPTYSALGGKIPIRWTAPPAIQRKFTASDVMSYGVIMVWVMSYGERPYWDMTN 857
QY 833 QDVINAIEQYRLPPPPMDPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKMRNPNSLKA 892
DB 858 QDVINAIEQYRLPPPPMDPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKMRNPNSLKA 917
QY 893 MAPLSSGINLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMED 952
DB 918 MAPLSSGINLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMED 977
QY 953 ILRLGVTLAGHQKILNSIQVMRAQMNQIQSVEV 986
DB 978 ILRLGVTLAGHQKILNSIQVMRAQMNQIQSVEV 1011

RESULT 12
ADO28627
ID ADO28627 standard; protein; 969 AA.
XX AC ADO28627;
XX 12-AUG-2004 (first entry)
XX DE Human EPHB2 protein SEQ ID NO:56.
XX KW high-grade dysplasia; HGD; oesophageal adenocarcinoma;
XX KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
XX KW EPHB2; chromosome 1.
XX OS Homo sapiens.
XX PN WO200404178-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036260.
XX PR 13-NOV-2002; 2002US-0425813P.
XX PA (GETH) GENENTECH INC.
XX PI Smith V;
XX DR WPI; 2004-420319/39.
XX DR N-PSDB; ADO28626.
XX

PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the genes.

XX Example 4; SEQ ID NO 56; 256pp; English.

XX The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predisposition of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC represents human EPHB2, which is used in the exemplification of the
CC present invention. The human EPHB2 gene is located on chromosome 1.

XX Sequence 969 AA;

Query Match 95.1%; Score 4936; DB 8; Length 969;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 969; Conservative 1; Mismatches 0; Indels 16; Gaps 16;

QY 2 ALRRLGAALLLLPLLAABVETLMDSTATAELGVMVHPSPGMEVSGYDENMTIRTYQV 61
DB 1 ALRRLGAALLLLPLLAABVETLMDSTATAELGVMVHPSPGMEVSGYDENMTIRTYQV 59
QY 62 CNVFESSQNNWLTKFIRRGARHIVEMKFSVRDCSSIPSVPGSCKETFNLYVYADFD 121
DB 60 CNVFESSQNNWLTKFIRRGARHIVEMKFSVRDCSSIPSVPGSCKETFNLYVYADFD 118
QY 122 SATKTFPNWNNENPWVVDITIADESQVLDLGRVNMKINTEVRSFGVSRSGFYLAQDY 181
DB 119 SATKTFPNWNNENPWVVDITIADESQVLDLGRVNMKIN- EVRSFGVSRSGFYLAQDY 177
QY 182 GGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYC 241
DB 178 GGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTS-VAARGSCIANAEVDVPKLYC 236
QY 242 NGDGWLVPIGRCMCKAGFEAVENGIVCRGCPSGT-KANQGDRACTHCPINSTRTSEGAT 301
DB 237 NGDGWLVPIGRCMCKAGFEAVENGIVCRGCPSGT- KANQGDRACTHCPINSTRTSEGAT 295
QY 302 NCVCNRYRDLPLDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSGREDLVNII 361
DB 296 NCVCNRYRDLPLDMPCTTIPSAQVAVISS- NETSLMLEWTPPRDSGREDLVNII 354
QY 362 CKSCGSGRGACTRCGDNVQAPRQLGLTEPRYIISDLAHTQYTFEIQAVNGVTDSPFS 421
DB 355 CKSCGSGRGACTRCGDNVQAPRQLGLTEPR- YISDLAHTQYTFEIQAVNGVTDSPFS 413
QY 422 PQFASVNIITNQAPSAVSIHQVSRITSLWSQDPQNGVILDYELQYERKELSEY 481
DB 414 PQFASVNIITNQAPSAVSIHQVSRIVD- ITLSWSQDPQNGVILDYELQYERKELSEY 472
QY 482 NATAIKSPNTVTVQGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKL 541
DB 473 NATAIKSPNTVTVQGLKAGAIYVQV- ARTVAGYGRYSGKMYFQMTAEAYQTSIQEKL 531
QY 542 PLIIGSAGLVFLIAVWIAIVCNRRGFERADSEYTDKLOHYSGHMTPGMKIYIDPFT 601
DB 532 PLIIGSAGLVFLIAVWIAIVCNRRGFERADSEYTDKLOHYSGHMTPGMKIYIDPFT 591
QY 602 YEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLKSQYTE 661
DB 592 YEDPNEAVREFAKEIDISCVKI- QVIGAGEFGEVCSGHLKLPGRKREIFVAIKLKSQYTE 650
QY 662 KORRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVI 721
DB 651 KORRDFLSEASIMQFDPN- IHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVI 709
QY 722 QLVGMRLGRTAAGMKYLADMYVHRDLAARNILVNSLVCKVSDGLSRFLEDDTSPTYT 781

Db 710 QLVGMLRGIAGMKYLAD-NYVHRDLAARNILVNSNLVCKVSDRGLRFLRDEDDTSDPTYT 768
Qy 782 SALGGKIPIRWTAPEAIQYRFTSASDWSYGIWVNEVMSYGERPYWDMNQDVINAIEQ 841
Db 769 SALGGKIPIRWTAPEA-QYRFTSASDWSYGIWVNEVMSYGERPYWDMNQDVINAIEQ 827
Qy 842 DYRLPPMDPCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGIN 901
Db 828 DYRLPPMDPCPSAL-QLMMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGIN 886
Qy 902 LPLDRTIPDYSFNTVDWLEALTKMGQYKESFANAGTSDVVSQMMEDILRLGYTLA 961
Db 887 LPLDRTIPDYT-FNTVDWLEALTKMGQYKESFANAGTSDVVSQMMEDILRLGYTLA 945
Qy 962 GHQKKILNSIOVRAQNMNQIOSVEV 986
Db 946 GHQKKILNSI-VRAQNMNQIOSVEV 969

RESULT 13

ADE63400
ID ADE63400 standard; protein; 984 AA.

XX ADE63400;

XX AC ADE63400;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein CAA31777, SEQ ID NO 9339.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-033347P.

XX PA (GEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX PR WPI; 2003-268312/26.

XX PR GENBANK; CAA31777.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX PR preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 984 AA;

Qy Query Match 75.8%; Score 3934.5; DB 7; Length 984;

Db Best Local Similarity 73.9%; Pred. No. 1.4e-287;

XX Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;

Qy 11 LLLPLLAAVEETLMDSTTAAELGMVHPHSGVEVSGYDENMNTIRTYQVNVFESSON 70

Db 10 LLASAVAAMEETLMDTRTAAELGWTANPASGVEVSGYDENLNTIRTYQVNVFEPNQ 69

Qy 71 NWLRTKEIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTPNW 130

Db 70 NWLLTTFINRRGARHRYTEMFTVRDCSSLPNPGCKETFNLYYYETDSVIATKSAFW 129

Qy 131 MENPWKVDITIAADESFQVDLGLRVKINTEVRSFGPVSRSFGYLAFOYGGCMSLIIV 190

Db 130 SEAPYLKVDITIAADESFQVDLGLRLMKVNTVRSFGLTRNGFYLAFOYGGCMSLSLV 189

Qy 191 RVFRRKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPV 250

Db 190 RVFFKKCPISIVQNFVFPETMTGAESTSLVIARGTCIPNAEVDVPIKLYCNGDGEWMPV 249

Qy 251 IGRCKAGFEAVENGTVCGPSCGTFKANQGBEACTHCIPINGRTTSEGATNCVCRNGYY 310

Db 250 IGRCTCKAGYEP-ENSIVACKACAPAGTFKASQEAEGCSHCPSNSRSPSEASPICTRCTGY 308

Qy 311 RADLDPLDMPCTTIPSAPOAVISSVNETSLMLBWTTPRDSGGREDLVYNIICKSGSGRG 370

Db 309 RADFDPEVACTSVPSGPRNVISIVNETSILBHPHPPRETGGRDDVYNIICKKCRADRR 368

Qy 371 ACTRCGDNVQYARQLGLTEPRIYISDLAHTQYTFEIQAVNGVTQSPSPFASVNIIT 430

Db 369 SCSCDDNVEFVPRQLGLTECRVSISSLWHTPTFDIQAINGVSSKSPFPQHVSNIT 428

Qy 431 TNOAAPSAVISIMHQVSRVDSITLSWSQPPQNGVILDYELQYKELSELYNATAIKSPT 490

Db 429 TNOAAPSVPIMHQVSATMRSITLSWPQEPQNGIILDYBIRYKEHEHNFNSMARSQT 488

Qy 491 NTVTVOGLKAGAIYVQVARTVAGYGRYKAYFOTMTEAEYQTSIQBKLPLIGSSAA 550

Db 489 NTARIDGLRPMGVYVQVARTVAGYKFGSKMCFQTLTDYDDEKSEUREQLPLIAGAAA 548

Qy 551 GLVFLIAVVVIAIVCNRRGFERADSEYTDKQHYTSGHMTFPGMKIYIDPTFYEDPNEAVR 610

Db 549 GVVFVSVLVAISVCSRKAYSKEAVYSKQHYSTGRSGPMKIYIDPTFYEDPNEAVR 608

Qy 611 EFAKEIDISCKIEQVIGAGEFGEVCSGHKLPGKREIFVAIKTLKSGYTEKORRDLSE 670

Db 609 EFAKEIDVSPKIEEIVIGAGEFGEVKGRLKPGKRIYVAIKTLKAGYSEKORRDLSE 668

Qy 671 ASTMGQFDHNVTHLGSVVTKSPVMIITFPMNGSLDSFLRNDQDGTFTVQLVGLMURGI 730

Db 669 ASIMGQFDHNVTHLGSVVTKSPVMIITFPMNGALDSFLRNDQDGTFTVQLVGLMURGI 728

Qy 731 AAGMKYLADNVYVHRDLAARNILVNSNLVCKVSDPGLRFLRDEDDTSDPTYSALGGKIP 790

Db 729 AAGMKYLSENVYVHRDLAARNILVNSNLVCKVSDPGLRFLRDEDDTSDPTYSALGGKIP 788

Qy 791 RWTAPAIQYRFTSADWSYGIWVNEVMSYGERPYWDMNQDVINAIEQDVLRLPPMD 850

Db 789 RWTAPAIYKKTASADVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 848
Qy 851 CPSALHQLMLDCWQKDRNRHFKGOIVNTLDKMTIRNPNSLKAMAPLSSGKLNPLDRTIP 910
Db 849 CPAALHQLMLDCWQKDRNSRFRFAEIVNTLDKMTIRNPASLKTATVATVAVPSQPLDPSIP 908
Qy 911 DYSFNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDILRLGVTLAGHQKILNS 970
Db 909 DFTAFITVDDWLSAIAKMWQYRDSFLTAGFTSLQVLTQWTSDELLRIGVTLAGHQKILSS 968
Qy 971 IQVMRAQWNOIQSV 984
Db 969 IHSRVRQWNOQSPSV 982

RESULT 14

AD83380
ID AD83380 standard; protein; 984 AA.

AC AD83380;

DT 29-JAN-2004 (first entry)

XX Rat Protein P09759, SEQ ID NO 10974.

DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.
XX GENBANK; P09759.

DR New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 984 AA;

Query Match 75.8%; Score 3934.5; DB 7; Length 984;
Best local Similarity 73.3%; Pred. No. 1.4e-287;
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;

Qy 11 LLLPLLAABEETLMDSTTATAELGMVHPHPSGWEVSGYDENNMNTIRTQVCNVFESSQN 70
Db 10 LLASAVAMEETLMDTATATAELGTANTPASGWEVSGYDENLNTIRTQVCNVFEPNQ 69
Qy 71 NWLRTKFIIRRGARHIVHEMKFSVRDCSSIPSPGSKCTFNLYYEADPSATKTFPNW 130
Db 70 NWLLTTFINRRGAHRIYTEMFTVRDCSSLPNVPGSKCTFNLYYEADPSATKTFPNW 129
Qy 131 MENPWKVDITIAADESFQVDLGGRYMKINTVRSFSPVSRSGFYLAFOYDYGCMSLIAV 190
Db 130 SEAPYLKVDITIAADESFQVDLGGRYMKINTVRSFSPVSRSGFYLAFOYDYGCMSLIAV 189
Qy 191 RVFRRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDDVPKILYCNCGDGEWLP 250
Db 190 RVFFKCPISIVQNFVFPETMTGAESTSLVIARGTCIPNAEEVDVDPKILYCNCGDGEWLP 249
Qy 251 IGRCMKAGFEAVENGTVRCGSPSTFKANQDEACTHCPINRSTTSEGATNCVCRNGYY 310
Db 250 IGRCTCKAGYEP-ENSVACKACPACTFKASQEAEGSCHPCSPNSRSPSEASPICTCTGY 308
Qy 311 RADLDPLDMPCTTIPSAPOAVISSVNETSLMLTWTTPRDSGGREDLVYNIICKSCSGRG 370
Db 309 RADFDPEVACTSPVSGPRNVISIVNETSLILSWHPRETGGRDDVTYNIICKCRADR 368
Qy 371 ACTRCGDNVQAPQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPFASVNIIT 430
Db 369 SCSCDDNVFVPRQLGLTECRVSISSLAHTPTFTDIAINGVSSKSPPPQHVSNIT 428
Qy 431 TNOAASAVSIMHOVSRTVDSITLWSQDPQNGVILDYELQYKELSEYNATATKSP 490
Db 429 TNOAAPTVPIMEHVSATWRSITLWSQDPQNGVILDYELQYKELSEYNATATKSP 488
Qy 491 NTVTVOGLKAGIYVQVRAARTVAGYRGYSGKMYFOTMTAEAYQTSIQEKLPIIGSSAA 550
Db 489 NTARIDGLRPGWVYVQVRAARTVAGYRGYSGKMYFOTMTAEAYQTSIQEKLPIIGSSAA 548
Qy 551 GLVFLIAVVIIVAIACNRRGFERADSEYTDKLQHYTSGHMTGPMKIYIDPPTYEDPNEAV 610
Db 549 GVVFVSVLVAISIVCSKRAYSKEAVYSDKLQHYTSGHMTGPMKIYIDPPTYEDPNEAV 608
Qy 611 EFAKEIDISCKIEQVIGAGEFGEVCSGHLKLPKKEIFVAIKTKSGYTEKORRDLSE 670
Db 609 EFAKEIDISCKIEQVIGAGEFGEVCSGHLKLPKKEIFVAIKTKSGYTEKORRDLSE 668
Qy 671 ASIMGQFDHPNVIHLEGVVTKSPVMIITEFMENGLDSFLRQNDQGFVTVQLVGMRLGI 730
Db 669 ASIMGQFDHPNVIHLEGVVTKSPVMIITEFMENGLDSFLRQNDQGFVTVQLVGMRLGI 728
Qy 731 AAGMKYLADNMYVHRDLAARNILVNSNLVKVSDFGLSRFLDDTSDPTYSALGKIKPI 790
Db 729 AAGMKYLSEMYVHRDLAARNILVNSNLVKVSDFGLSRFLDDTSDPTYSALGKIKPI 788
Qy 791 RWTAPAIYKKTASADVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 850
Db 789 RWTAPAIYKKTASADVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 848
Qy 851 CPSALHQLMLDCWQKDRNRHFKGOIVNTLDKMTIRNPNSLKAMAPLSSGKLNPLDRTIP 910
Db 849 CPAALHQLMLDCWQKDRNSRFRFAEIVNTLDKMTIRNPASLKTATVATVAVPSQPLDPSIP 908

```
Qy 911 DYTSTNTVDEWLEAKNQYKESFANAGTSTFDVVQMMEDILRLGVTLGAGHOKKILNS 970
Db 909 DFTAFTTVDWLSAIAKMWQYRDSFLTGTSLQVLTQWTSDDLRLGVTLAGHOKKILSS 968

Qy 971 IQVRAQWNIQSV 984
Db 969 IHSNRVQWQNSPSV 982

RESULT 15
AAR44513
ID AAR44513 standard; protein; 984 AA.
XX AC
XX AAR44513;
XX DT 16-JUN-1994 (first entry)
XX DE elk.
XX KW Lambda gt11; expression vector; lambda-BI-Elk; protein tyrosine kinase;
XX KW Elk; B1; Eph; subfamily; receptor-like tyrosine kinase; eph; eck;
XX KW phosphorylation; phosphorylated kinase insert domain; growth factor;
XX KW receptor kinase; platelet-derived growth factor receptor.
XX OS Rattus rattus..
XX PH
XX Key Location/Qualifiers
XX Peptide 1..17 "Signal peptide"
XX FT Misc-difference 61 /note= "Cysteine residue"
XX FT Misc-difference 96 /note= "Cysteine residue"
XX FT Misc-difference 106 /note= "Cysteine residue"
XX FT Misc-difference 183 /note= "Cysteine residue"
XX FT Misc-difference 196 /note= "Cysteine residue"
XX FT Misc-difference 225 /note= "Cysteine residue"
XX FT Misc-difference 240 /note= "Cysteine residue"
XX FT Misc-difference 253 /note= "Cysteine residue"
XX FT Misc-difference 255 /note= "Cysteine residue"
XX FT Misc-difference 267 /note= "Cysteine residue"
XX FT Misc-difference 270 /note= "Cysteine residue"
XX FT Misc-difference 284 /note= "Cysteine residue"
XX FT Misc-difference 287 /note= "Cysteine residue"
XX FT Misc-difference 301 /note= "Cysteine residue"
XX FT Misc-difference 303 /note= "Cysteine residue"
XX FT Misc-difference 319 /note= "Cysteine residue"
XX FT Misc-difference 360 /note= "Cysteine residue"
XX FT Misc-difference 363 /note= "Cysteine residue"
XX FT Misc-difference 370 /note= "Cysteine residue"
XX FT Misc-difference 373 /note= "Cysteine residue"
XX FT Modified-site 425..427 /note= "N-glycosylation site"
XX FT Modified-site 480..482
```

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FT XX /note= "N-glycosylation site"
PN XX CA2083521-A.
XX XX 01-OCT-1993.
XX XX 23-NOV-1992; 92CA-02083521.
XX XX 31-MAR-1992; 92US-00861390.
XX XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX XX Pawson A, Reedijk M, Letwin K;
XX XX WPI; 1993-406300/51.
XX XX N-PSDB; AAQ53471.
XX XX Expression of phosphorylated exogenous protein - in host cells
XX XX catalytic domain of protein kinase.
XX XX Disclosure; Fig 3; 55pp; English.
XX CC This sequence is encoded by the elk cDNA and represents the protein
XX CC tyrosine kinase, Elk. The Elk gene, B1, encode a protein which is a
XX CC member of the Eph subfamily of protein tyrosine kinases. The Elk product
XX CC is very similar to two other receptor-like tyrosine kinases, eph and eck.
XX CC Lambda-BI-Elk may be used in the production of phosphorylated exogenous
XX CC protein along with a further vector encoding the desired exogenous
XX CC protein. These plasmid may be used to produce phosphorylated proteins in
XX CC host cells which have no intrinsic capacity for phosphorylation, eg.
XX CC bacteria. The system may be used for the expression of the phosphorylated
XX CC kinase insert domain of a growth factor receptor kinase eg. platelet-
XX CC derived growth factor receptor
XX XX
XX SQ Sequence 984 AA;

Query Match 75.7%; Score 3926.5; DB 2; Length 984;
Best Local Similarity 73.8%; Pred. No. 5.7e-287;
Matches 719; Conservative 128; Mismatches 126; Indels 1; Gaps 1;

Qy 11 LLLPLAAVETLMDSTTATAEILGWMVHPSPGSEVSGYDENMTTIRTYQVGVFESSON 70
Db 10 LLASAVAAMEETLMDTATAEILGWTANPASGSEVSGYDENLNTIRTYQVGVFEPNQ 69
Qy 71 NWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYYEADSDATKTPPW 130
Db 70 NWLTFITRRGAHRIYTEMRFVDRDCSSLPNVPGSKETFNLYYYETSDVIATKSAFW 129
Qy 131 MENPWKVDITAADESFSQVDLGGVRVMKINTEVRSFGPVSRSFGYLAFOYGGCMSLI 190
Db 130 SEAPYLKVDITAADESFSQVDLGGRLMKVNTVRSFGPLTRNGFYLAFOYGACMSLLSV 189
Qy 191 RVFYKCPRIQNGAIFQETLSGAESTSLVAAGSCIANAEVDVDPKLYCNGDGEWLP 250
Db 190 RVFFKKCPISIVQNFVAVPETMTGAESTSLVIARGTCPNABEVDVDPKLYCNGDGEWMP 249
Qy 251 IGRMCKAGPEAVENGTVCRGCPSTFKANQGEACTHCPINRSITSEGATNCVCRNGY 310
Db 250 IGRCTKAGYEP-ENSVACKACPAGTFKASQEAEGCHGCHSPNSRSPSEASPTCTRGY 308
Qy 311 RADLDPLDMPTCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCSGRG 370
Db 309 RADFDPEVACTSVPSGPRNVISIVNETSIILEMPPRETGGRDDVTYNIICKCRADR 368
Qy 371 ACTRCGDNVOYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSQPASVNI 430
Db 369 SCSCDDNVFVRQLGLTECRVSISSLWAHTYTFDQIAINGVSSKSPSPQHVSNIT 428
Qy 431 TNOAAPSASVIMHOVSRTVDSITLSKQSDPQNGVILDYELQYVEKELSEVNAITAKPT 490
Db 429 TNOAPSTVPIMHQVSATMRSEITLSWPQEPQNGIILDYEIRYIEKEHNEFNSMARSQT 488
```

	QY	491	NTVTVOGLKAGAIYVQVRARTVAGYGRYSCKMYFQTMTAEAYQTSIQEKLPLIICTSSAA	555
	DQ	489	NTARIDGLRPGMVGVIYVQVRARTVAGYKFGSKMSFOTLTDDDYYIKSELREBQLPIIAGSAAA	548
	QY	551	GUVLFLIAVVVTAIVCNRRGPERADSEYTKLQHVTYSGHMTPGMKIYIDPPTYEDPNEAVR	610
	DB	549	GVVFVSILVAISIVCSRKAAYSKEAIVSDKLQHYSTGRGSPGMKIYIDPPTYEDPNEAVR	608
	QY	611	EPAKEIDSCVKIEOVI GAGBEFGEVCVSHLKLPGKREIFVAIKTLKSGYTEKKORRDPLSE	670
	DB	609	EPAKEIDSVFKIEEVI GAGBEFGEVYKGRLLKLPKGREIYVAIKTLKAGYSEKKORRDPLSE	668
	QY	671	ASIMGQFDHPNVHLHLEGGVYKSTPMIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLGI	730
	DB	669	ASIMGQFDHPNIIRLEGVYTKSRPMIITEFMENGALDLSFLRQNDGQFTVIQLVGMRLGI	728
	QY	731	AAGMKYLADMNYVHRDLAARNILVNSNLVCKVDFGLSFLEDDTSDPTVTSALGKGKIP	790
	DB	729	AAGMKYLSMMNYPVHRDLAARNILVNSNLVCKVDFGLSYLVLDQDTSDPTVTSLSLGKIPV	788
	QY	791	RWTAPETAYRKFTSASDVWSYGIVMMEVNSYGERPYMDTNODVINATIEDYRLPPMD	850
	DB	789	RWTAPETAIRKFTSASDVWSYGIVMMEVNSYGERPYWDMNSQDVINATIEDYRLPPMD	848
	QY	851	CPSALHQMLMLDCWKQRNHRPKFGQIVNTLDMIRNPNSLKAMAPLSSGINLPLDRTIP	910
	DB	849	CPAALHQMLMLDCWKQRNRPRAEIVNTLDMIRNPASLKTVAITAVPSQPLLDRSIP	908
	QY	911	DVTSFNVTDEWLBAIKMGQYKESFANAGFTSFVDVVSOMMEDILRLGVTLAGHKILNS	970
	DB	909	DFTAFTVDDWMLSAIRMVQYRDSFLTAGFTSLQLVTQMTSEDLLRIGVTLAGHKILNS	968
	QY	971	IQMVBQAQMNQIOSV 984	
	DB	969	IHSMRVMQNQSPSV 982	
		RESULT 16		
		ADE83382		
		ID ADE83382 standard; protein; 984 AA.		
		XX AC ADE83382;		
		XX DT 29-JAN-2004 (first entry)		
		XX DE Human Protein P54762, SEQ ID NO 10976.		
		XX KW Human; pain; neuronal tissue; gene therapy;		
		KW spinal segmental nerve injury; Chronic constriction injury; CCI;		
		KW spared nerve injury; SNI; Chung.		
		XX OS Homo sapiens.		
		PN WO2003016475-A2.		
		XX PD 27-FEB-2003.		
		XX PF 14-AUG-2002; 2002WO-US025765.		
		XX PR 14-AUG-2001; 2001US-0312147P.		
		PR 01-NOV-2001; 2001US-0346382P.		
		PR 26-NOV-2001; 2001US-0333347P.		
		XX (GENO) GEN HOSPITAL CORP.		
		PA (FARB) BAYER AG.		
		PI Woolf C, D'urso D, Befort K, Costigan M;		
		XX WFI; 2003-268312/26.		
		XX GENBANK; P54762.		
		XX New composition comprising two or more isolated polypeptides, useful for		
		PT preparing a medicament for treating pain in an animal.		

Qy 541 LPLIGSSAAGLVFLIAVWVIAIYVNCRRGFERADSEYDVKLQHYTSGHMTPGMKIYIDPF 600
Db LPLIAGSAAAGVFWVSLVAISIVCSRKRAYSKAVYSDKLQHYSTGSGPMKIYIDPF 598
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 660
Db 599 TYEDPNEAVREFAKEIDISFVKIEBIVIGAGEFGEVYKGRLLPKGRBIYVAIKTLKAGYS 658
Qy 661 EKORRDLSEASIMGQFDHPNVIHLGVVTKSTPVMIIITFEMENGSLDSFLRQNDGQFTV 720
Db 659 EKORRDLSEASIMGQFDHPNIRLEGVVKSRPVMIIITFEMENGALDSFLRQNDGQFTV 718
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRLEDDTSPTY 780
Db 719 IQLVGMRLGIAAGMKYLAEMNYVHRDLAARNILVNSNLVCKVDFGLSRVLDQDTSPTY 778
Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGRPYWDMTNOVDVINAIE 840
Db 779 TSALGGKIPVRWTAPEAIYRKFTSASDVMSYGIWMEVMSYGRPYWDMTNOVDVINAIE 838
Qy 841 QDYRLPPMDPCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSKAMAPLSSGI 900
Db 839 QDYRLPPMDPCPALHQLMLDCWQKDRNSRPRFAEIVNTLDMKIRNPNLSKATVATIPV 898
Qy 901 NLPLDRTIPDYTFNTVDEWLEIAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960
Db 899 SQPLDLSIPDFTAFITVDWLSAIKMWQVYRDSFLTAGFTSLQLVTQWTSDELIRIGITL 958
Qy 961 AGHOKKILNSIQVMRAQMNQ 980
Db 959 AGHOKKILNSIHSRMVQISQ 978

RESULT 17

ADFO9563
ID ADFO9563 standard; protein; 984 AA.

XX AC ADFO9563;

XX DT 12-FEB-2004 (first entry)

XX DE Human EphA1 SEQ ID NO:64.

XX KW human; protein-protein interaction; virucide; cytostatic; vaccine;
KW human papilloma virus; HPV; cancer.

XX OS Homo sapiens.

XX PN W02003068940-A2.

XX PD 21-AUG-2003.

XX PF 14-FEB-2003; 2003WO-US004594.

XX PR 14-FEB-2002; 2002US-0356911P.

XX PA (CURA-) CURAGEN CORP.

XX PA (HOFF) HOFFMANN LA ROCHE INC.

XX PI Jackson A, Ooi CE, Lewin DA, Cuthill S;

XX DR WPI; 2003-689668/65.

XX DR N-PSDB; ADFO9670.

XX PT New purified complex comprising a first polypeptide and a second
PT polypeptide, useful for identifying agents for treating/preventing a
PT condition involving altered level of the complex e.g. human papilloma
PT virus infection, or cancer.

XX PS Example 3; SEQ ID NO 64; 156pp; English.

XX CC The invention relates to a novel purified complex comprising a first
CC polypeptide and a second polypeptide, where the polypeptides comprise

CC defined amino acid sequences listed in the specification, and where the
CC first polypeptide binds to the second polypeptide. A complex of the
CC invention has virucide and cytostatic activity, and may have a use as a
CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADFO9500-ADFO9583 represent proteins of the
CC invention.

XX SQ Sequence 984 AA;

Query Match 75.6%; Score 3924; DB 7; Length 984;
Best Local Similarity 73.5%; Pred. No. 8.8e-287;
Matches 720; Conservative 130; Mismatches 128; Indels 2; Gaps 2;

Qy 1 MALRRGCAALLPLLAAVEETLMDSTATAELGVMVHPSPGMEVSGYDENMTITTYQ 60
Db 1 MALDYL-LLLLASAAVAMEETLMDTRTATAELGWTANPASGMEVSGYDENLMTITTYQ 59
Qy 61 VCNVFESSQNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVPGSKCTFNLYYYEADF 120
Db 60 VCNVFEPNQNNWLLTTFINRGAHRIYTEMFTVRDCSSLPNVPVPGSKCTFNLYYYETDS 119
Qy 121 DSATKTFPNMNMWPKVDTIAADESFQVDLGGRVKMKINTEVRSPGVSRSGFYLAQD 180
Db 120 VIATKSAFSEAPYLKVDITIAADESFQVDLGGRLMKVNTVRSFGPLTRNGFYLAQD 179
Qy 181 YGCMSLIAVRFYRKCPRIIONGATFOETLSGAESTSLVAARGSCIANAEVDVPTKLY 240
Db 180 YGACMSLLSVRFVFKCPSIVQNFAPFETMTGAESTSLVIARGTCIPNAEEVDVPTKLY 239
Qy 241 CNGDGWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINRSTTSEGA 300
Db 240 CNGDGEMWPIGRCTCKPGYEP-ENSVAACKACAGTFKASQEAEGCHCSNSRSPAES 298
Qy 301 TNCVCRNGYYRADLPLDMPCTTIPSAQAVISVNETSLMLBWTTPRDSGGREDLYNI 360
Db 299 PICTCRGTYYRADFPPEVACTSVPSGPRNVISIVNETSIILEWHPPRETGGRDVYNI 358
Qy 361 ICKSCSGRCACCTCGDNVQYAPROGLTEPRYIYDILLAHQYTPRIQAVNGVTDOSPF 420
Db 359 ICKKCRADRRSCRCDDNVFVPRQGLTECRVISLSLWHTPTPTDQAINGVSSKSPF 418
Qy 421 SPOFASVNTTNOAAPSASVIMHQVSRVTDSITLSWSQDPQPNQVILDYELQYKEKELSE 480
Db 419 PPQHVSVNTTNOAAPTSTVPMHQVSATMPSITLSWPPQPNQVILDIYIRIYKEHNE 478
Qy 481 YNATAKSPNTVTVOGLKAGAIYVFQVARTVAGYRGYSGKMYFQMTBAEYQTSQEK 540
Db 479 FNSSMARSQNTARIDGLRPGMVVYVQVRAARTVAGYKFGSKMKCFQTLTDDYKSELREQ 538
Qy 541 LPLIGSSAAGLVFLIAVWVIAIYVNCRRGFERADSEYDVKLQHYTSGHMTPGMKIYIDPF 600
Db 539 LPLIAGSAAAGVFWVSLVAISIVCSRKRAYSKAVYSDKLQHYSTGSGPMKIYIDPF 598
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 660
Db 599 TYEDPNEAVREFAKEIDISFVKIEBIVIGAGEFGEVYKGRLLPKGRBIYVAIKTLKAGYS 658
Qy 661 EKORRDLSEASIMGQFDHPNVIHLGVVTKSTPVMIIITFEMENGSLDSFLRQNDGQFTV 720
Db 659 EKORRDLSEASIMGQFDHPNIRLEGVVKSRPVMIIITFEMENGALDSFLRQNDGQFTV 718
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRLEDDTSPTY 780
Db 719 IQLVGMRLGIAAGMKYLAEMNYVHRDLAARNILVNSNLVCKVDFGLSRVLDQDTSPTY 778
Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGRPYWDMTNOVDVINAIE 840
Db 779 TSALGGKIPVRWTAPEAIYRKFTSASDVMSYGIWMEVMSYGRPYWDMTNOVDVINAIE 838
Qy 841 QDYRLPPMDPCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSKAMAPLSSGI 900

```
Db 839 QDYRLPPMDCPAALHQLMLDCWKDRNSRPRFAEIVNTLDKMRNPASLKTATITAVP 898
Qy 901 NLPILDRITPTYSFNTVDEWLEIAIKGOYKESFANAGFTSFVVSOMMEDILRLGVTL 960
Db 899 SLPILDRISIPDFTFTTVDWLSAIRMVQYRDSFLTAGFTSLQLVQTWTSDDLRLIGITL 958
Qy 961 AGHOKILNSIQVMRAQMNQ 980
Db 959 AGHOKILNSIHSNRVQISQ 978

RESULT 18
ID AAR75704 standard; protein; 951 AA.
XX AAR75704;
AC AAR75704;
XX 25-MAR-2003 (revised)
DT 11-NOV-1995 (first entry)
XX
XX Eph-related CEK6.
XX
XX CEK6; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis; prognosis.
XX
XX Gallus sp.
XX
XX Key Location/Qualifiers
XX Domain 426..444
XX /label= Extracellular_domain
XX
XX WO9515375-A1.
XX
XX 08-JUN-1995.
XX
XX 07-SEP-1994; 94WO-US010140.
XX
XX 03-DEC-1993; 93US-00162809.
XX
XX (LJOL-) LA JOLLA CANCER RES FOUND.
XX
XX Pasquale EB, Sajjadi FG;
XX
XX WPI; 1995-215256/28.
XX N-PSDB; AAQ90652.
XX
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
XX cancer.
XX
XX Claim 12; Page 37-41; 129pp; English.
XX
XX Novel Eph-related PTK Cdk6 cDNA clones (AAQ90652) were isolated from
XX chick embryo and embryonic brain cDNA libraries in phage lambda gt11. The
XX encoded Cdk6 protein (AAR75704) is closely related to rat Elk, Cdk6
XX (AAR75712) and Cdk10 (AAR75708). Cdk6 transcripts were found in 10-day
XX embryos and in adult brain, lung, heart and skeletal muscle. (Updated on
XX 25-MAR-2003 to correct PN field.)
XX
XX Sequence 951 AA;
XX
Query Match 71.6%; Score 3715.5; DB 2; Length 951;
Best Local Similarity 70.2%; Pred. No. 4.6e-271;
Matches 687; Conservative 121; Mismatches 118; Indels 53; Gaps 3;
Qy 21 ETLMDSTATAELGMMVHPSPGSEVSGYDENMTTIRTYQVCNVFESSONMLRTKPIR 80
Db 1 ETLMDTATAELGMMVHPSPGSEVSGYDENMTTIRTYQVCNVFEPNQNMLLTPIR 60.
Qy 81 RGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEADFDSATKTPPNMNMENPWKVD 140
Db 61 RGAHRIYTEMFTVRDCSSLPNPGSKCTFNLYYYWTDVSDVIATKKSFAFWTEAPYLKVD 120
Qy 141 IAADESFQVDLGGVRMKNTEVRSFGPVSRSFGYLAQDYGGCMSLIAVRVYRKPRI 200
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Db 121 IAADESFQVDYFGRLMK-----GFFKKCPV 147
Qy 201 IQNGALPQETLSAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKAGF 260
Db 148 VONFAIPPETMTGAESTSLVARTGTCIPNAEEVDVPIKLYCNGDGEWLVPIGRCTKAGY 207
Qy 261 EAVENGTCVCGSGTFCANQGDCAETHCPINSRTTSEGATNCVCRNGVYRADLDPLDMP 320
Db 208 EP-ENNACACACAGTFCASQAGLCAACPCPNRSSAEASPLCACRNGYFRADLDPTAA 266
Qy 321 CTTIPSAQAIVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRCACTRCGDNVQ 380
Db 267 CTSVPSGPRNVISIVNETSILLENWPPRETGGDDVTYNIIVCKCRADRCACRCDNVE 326
Qy 381 YAPQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNIITNOAAPSASV 440
Db 327 FVPQLGLTETRVFISLWHTPTTFEIQAVNGVSNKSPFPQHVSVNITNOAAPSSTVP 386
Qy 441 IMHQVSRVTDSITLSWSQDOPNGVILDYELQYK-----ELSEY 481
Db 387 IMHQVSATMRSITLSWPPQEPQNGIILDYELRYEKLRICTPDVSGTVGSRRAADHNEY 446
Qy 482 NATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGMYFQWTAEAYQTSIQEKL 541
Db 447 NSSVARSQNTARLEGLRPGMVYVQVRAFTVAGYKYSKMCFOITLDDYKSELREQL 506
Qy 542 PLIIGSAGLVPLIAVVIAIVCNRRGPERADSEYTDKLOHTSGHMTPGMKIYIDPFT 601
Db 507 PLIAGSAGLVPLIIVSVAISIVCSRKRAYSVVYSDKLOHYSTGRGSPGMKIYIDPFT 566
Qy 602 YEDPNEAVREFAKEIDISCVKIQVIGAGFEGVCSGHLKLPGRKELFVAIKLKSQYTE 661
Db 567 YEDPNEAVREFAKEIDVSVFKIEVIGAGFEGVYKGRKLPGRRIYVAIKLKGAYSE 626
Qy 662 KORRDFLSEASIMGQFDHPNVHLEGVTKSTPMIITEFMENGSLDSFLRQNDGQFTVI 721
Db 627 KORRDFLSEASIMGQFDHPNIIRLEGVTKSRPMIITEFMENGALDSFLRQNDGQFTVI 686
Qy 722 QLVGMLRGTAAGMKYLADNMVYHRDLAARNILVNSLVCKVSDPGLSRLEDDTSDPTYT 781
Db 687 QLVGMLRGTAAGMKYLAEMNYVHRDLAARNILVNSLVCKVSDPGLSRVLDQDTSPTYT 746
Qy 782 SALGGKIPRTWTAPEAIQYRKFTSASDVMSYGVIMVMSYGERPYWDMTNQDVINAIEQ 841
Db 747 SSLGGKIPRTWTAPEAIYRKFTSASDVMSYGVIMVMSYGERPYWDMNSQDVINAIEQ 806
Qy 842 DYRLPPMDCPSALHQLMLDCWKQDRNHRPKFGQIVNTLDKMRNPNSLAKAMAPLSGIN 901
Db 807 DYRLPPMDCPSALHQLMLDCWKQDRNTRPRLAEIVNTLDKMRNPASLKTATITAVPS 866
Qy 902 LPLLDRTIPDYTSFNTVDEWLEIAIKGOYKESFANAGFTSFVVSOMMEDILRLGVTLA 961
Db 867 QPLDLSIPDFTFTTVDWLSAIRMVQYRDSFLTAGFTSLQLVQTWTSDDLRLIGITL 926
Qy 962 GHOKILNSIQVMRAQMNQ 980
Db 927 GHOKILNSIQSRVQMSQ 945

RESULT 19
ADN39865
ID ADN39865 standard; protein; 998 AA.
XX
XX ADN39865;
AC ADN39865;
XX
XX 17-JUN-2004 (first entry)
XX
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C235.
XX
XX Human; differential expression; cancer; angiogenic disorder;
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
XX inflammatory disease; autoimmune disease;
```


retinal neovascularisation syndrome; scarring; uterine fibroid;
detection; diagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine.

Homo sapiens.

W02003042661-A2.

22-MAY-2003.

13-NOV-2002; 2002WO-US036810.

13-NOV-2001; 2001US-0350666P.

21-NOV-2001; 2001US-0332464P.

29-NOV-2001; 2001US-0334393P.

03-DEC-2001; 2001US-0335394P.

14-DEC-2001; 2001US-0340376P.

08-JAN-2002; 2002US-0347211P.

10-JAN-2002; 2002US-0347349P.

08-FEB-2002; 2002US-0355250P.

13-FEB-2002; 2002US-0356714P.

20-FEB-2002; 2002US-0359077P.

29-MAR-2002; 2002US-0368809P.

04-APR-2002; 2002US-0370110P.

12-APR-2002; 2002US-0372246P.

05-JUN-2002; 2002US-0386614P.

16-JUL-2002; 2002US-0396839P.

22-JUL-2002; 2002US-0397775P.

22-JUL-2002; 2002US-0397845P.

09-SEP-2002; 2002US-0409450P.

(E0SB-) EOS BIOTECHNOLOGY INC.

Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

WPI; 2003-468649/44.

N-PSDB; ADN39648.

Determining the presence or absence of a pathological cell in a patient,
useful for diagnosing, prognosing or treating cancer, comprises detecting
a nucleic acid in a biological sample.

Claim 12; SEQ ID NO C235; 1385pp; English.

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides, and
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularisation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a polypeptide of the invention.

Sequence 998 AA;

Query Match 70.7%; Score 3670.5; DB 7; Length 998;

Best Local Similarity 70.4%; Pred. No. 1.2e-267;

Matches 694; Conservative 115; Mismatches 158; Indels 19; Gaps 6;

10 LLLPL-----AAVETLMDSTATAELGWMVHPSPGWEVSGYDENMNTINTYQVCN 63

23 LLLPLLLPAGCRALETLMDTKWTSELAWTSHPSGWEVSGYDENMNTINTYQVCN 82

Qy	64	VRESSQNNWLRTKFIERRGAHRHIVEMKFSYRDCSSIPSPGCKETFNLYYYEADFDA	123
Db	83	VRESSQNNWLRTGFIERDVRQVYVELKFTVRDCNSIPNIPGCKETFNLYYYEADSDVA	142
Qy	124	TKTFPNWMPWVKVDITIAADESFQVDLGRVWKINTEVRSPGVSRSGLYAFQDYGG	183
Db	143	SASSPFWMENPYKVDITIADESFRLDAG----RVNTKVRSFGSLKAGFYLAFOQGA	198
Qy	184	CMSLIAVRVFRKCPRIIQNGAIFOETLSGAESTSLVAARGSCIANAEEDVPIKLYCNG	243
Db	199	CMSLISVRIFYKKCASTAGTALFPETLTGAETSLVIAPGTCTPNAVEVSVPKLYCNG	258
Qy	244	DGEWLVPIGRCMKCKAGFEAVENGTVCRGCPSTGTFKANKQGDCACTHCPINSTRTTSE	303
Db	259	DGEWVPVGACTCATGHEPAKESQCRPCPGSYKAKQGGPCPLPCPNSTRTTSPAASIC	318
Qy	304	VRNGYYRADLDPLDMPCTTIPSAQAVISVNETSLMLEWTPPRDGGREDLYNICK	363
Db	319	TCHNFFYRADSDSADSACTTVPSPRGVIVNNVNETSLILEWSEPRDLGGRDDLLYNV	378
Qy	364	SC--GSGRGACTRCGDNVQAPROLGTEPRIVYISDLAHTQYTFEIQAVNGVTDQSP	421
Db	379	KCHGAGGASACRCDNDNVEFVPQLGLTERRVHLLAHTRYTFEQAVNGVSGKSLP	438
Qy	422	QPFASVNITNQAAAPSASVIMHQSRTVDSITLWSQDQDPNGVILDYQYVEKELSEY	481
Db	439	PRVAVNITNQAAAPSEVPTLRHSSGSLTSLWAPPERPENGVLIDYEMKYFEK--SB	496
Qy	482	NATAIKSPNTVTVQGLKAGAIYVQVARTVAGYSGMYQFQWTE-ABYQTSIQEK	540
Db	497	IASTVTSQMSVQLDGLRPDARYVQVARTVAGYSGYSPAEFTTSSRGSAQQLQEQ	556
Qy	541	LPLIIGSSAAGLYFLIAVVIATVNCNRRGERADSEYDKLOHYTSGHMTGMYIDPF	600
Db	557	LPLIVGSATAGLVFVAVVIAIVCLRKQHGSDSEYTELQYQY----IAPGMKYIDPF	612
Qy	601	TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKIFVIAIKLKG	660
Db	613	TYEDPNEAVREFAKEIDVSCVKIEEVIGAGEFGEVCGRLKQGRREVFAIKLVGYT	672
Qy	661	EKQRDPFLSASIMQGDHPNVHLEGVVTKSTPVMITTFEMNGSLDSFLRQNDGQFTV	720
Db	673	ERQRDPFLSASIMQGDHPNIIIRLEGVTKSRPVMILTTFMENCALDSFLRLNDGQFT	732
Qy	721	IQLVGLRGTAAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLDDTSQPT	780
Db	733	IQLVGLRGTAAGKYLSENNYVHRDLAARNILVNSLVCKVSDFGLSRFLDDTSQPT	792
Qy	781	TSALGGKIPRTWTAPEAIQVKTFSASDVMSYGVIMVMSYGBRPYDMTQDVINAIE	840
Db	793	TSSLGGKIPRTWTAPEAIYRKFTSASDVMSYGVIMVMSYGBRPYDMTQDVINAIE	852
Qy	841	QDYRLPPMDPCPSALHQLMDCQKDRNHRPKFQIVNTLDKRMNPNLSLKAMAPLSSGI	900
Db	853	QDYRLPPMDPCPSALHQLMDCVVRDRNLRPKFSQIVNTLDKLRNAASLKVIAAQSGM	912
Qy	901	NLPDLRTIPTYTSFNTVDWLEIAIKGQYKESFANAGFTSFVVSOMMEDILRLGVT	960
Db	913	SQPLDRTVPTYTFTTFTVGDWLDIAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIG	972
Qy	961	AGHQKILNSIQVMRAQMNQIQSVEV 986	
Db	973	AGHQKILNSIQVMRAQMNQIQSVEV 998	
RESULT 20			
AAR75708			
ID	AAR75708	standard; protein; 973 AA.	
XX			
XX	AAR75708;		
DT	25-MAR-2003	(revised)	

CC Novel EPH-related PTK cDNA clone Cek10 (given in AAQ90656) and a variant
CC clone, Cek10+ (AAQ90658), whose product contains a 15-amino acid
CC insertion in the juxtamembrane domain, were isolated from a chick embryo
CC library in lambda gt11. Cek10 and Cek10+ may originate from the same gene
CC by alternative splicing. Cek10 expression was prominent in the kidney,
CC and to a lesser extent in the lung. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 988 AA;

Query Match 70.6%; Score 3662.5; DB 2; Length 988;
Best Local Similarity 70.1%; Pred. No. 4.9e-267;
Matches 684; Conservative 121; Mismatches 144; Indels 27; Gaps 5;

Qy 30 TAEIGMWHVPPSGWEEVSGYDENNTIRTYQCVNFESSQNMLRTKFIKRRGAHRIHVE 89
Db 21 TSELATWTHETGWEVSGYDEANPIRTYQCVNREANQNWLRTKFIQRDVQRVVE 80

Qy 90 MKFSVRDCSSIPSPVSGCKETFNLYYYEADPDSATKTFPNMNMENWVKVDTIAADESFSQ 149
Db 81 LKFTVRDCNIGTNPISGCKETFNLYYYEADPDSATKTFPNMNMENWVKVDTIAADESFSK 140

Qy 150 VDLGGRVMKNTVRSRGPVSRSGFYLAFOGYGCMSLIARVRYFKCPRIIONGAIFOE 209
Db 141 LESG----RVNTKVRSGPLSKNGFYLAFOQDLGACMSLISVRAPYKCSNTIAGFAIPPE 196

Qy 210 TLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDGEWLVPIGRCMKCAGFEAVENGTVG 269
Db 197 TLTAETPSLVIAPGTCTPNAVEVSPLKLYCNGDGEWVPGACTCAAGYEPAMKDTQC 256

Qy 270 RGCPSGTFKANQDEATHCPINSRTTSEGATNCVCRNGYYRADLPLDMPTCTTIPSAQ 329
Db 257 QACPGPTFKSQGPGCPSPNRTTAGAATVTCICRSGPFRADADPADSACTSVPSAPR 316

Qy 330 AVISSVNETSLMLEWTPRDSGGREDLVNIIKSCSGRGCACTRCGDNVQYAPROL--- 386
Db 317 SVISNVNETSLVLEWSEFQDAGGRDGLLYNVICKCSVERRLRCDDNVFEFVQLGLT 376

Qy 387 GLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPOFASVNTTNOAPSASVSIHQVS 446
Db 377 GLTEPRYIYSKVMAHPQYTFEIOAVNGISKSPPPHFASVNTTNOAPSASVPTMLHS 436

Qy 447 RTVDSITLSWSQDPQNGVILDVLOYEKE-ISEYNATAIKSPNTVTVOGLKAGAIYV 505
Db 437 STGNSMTLSWTPPRNGIILDEIKYSEKQGGDGIANTVTSQNSVRDLGLKANARYM 496

Qy 506 FOVRARTVAGRYSGMYQTMTEAEYQTSIQEKLPIILIGSSAAGLVFLIIVVIAIVC 565
Db 497 VQVRARTVAGRYSLPTEPQTAECDGSTSKTFOELFLVGSATAGLLFVIVVIAIVC 556

Qy 566 NRRGF-----ERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAVR 610
Db 557 FRKGWTEQLLSPLGRKQNSDTPETEKLOQY----VTPGKVIYIDPFTYEDPNEAVR 612

Qy 611 EFAKEIDISCKIEQVITGAGEFVCSGHLKLPKREIFVAIKTLKSGYTEKQRDPFSE 670
Db 613 EFAKEIDISCKIEVITGAGEFVCSGRLKLPGRREIFVAIKTLKVGYTEKQRDPFSE 672

Qy 671 ASINGQFDHNVHLEGVTKSTPVMIIIFEMENGLSDSLRQNDGQFTVQLVGLMGI 730
Db 673 ASINGQFDHNIHLEGVTKSRPVMIIIFEMENCALDSFLRLNDGQFTVQLVGLMGI 732

Qy 731 AAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSPTYSALGGKIPI 790
Db 733 AAGKYLSEMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDPADPTYSALGGKIPI 792

Qy 791 RWTAPAEIQRKFTSASDWSYGIYVMWVMSYGRPYWDMTNQDVINAIBQDYRLPPMD 850
Db 793 RWTAPAEIQRKFTSASDWSYGIYVMWVMSYGRPYWDMNSQDVINAVEQDYRLPPMD 852

Qy 851 CPSALHQLMDCWQDRNRHPRKFOIYNTLDKMTIRNPNSLKAMAPLSSGILNPLDRTIP 910
Db 853 CPTALHQLMDCWVRDRNRHPRKFAQIYNTLDKLRNAASLKVIASVQSGVSQLDRTVP 912

Qy 911 DYTSFNTVDWLBAIKMGQYKESFANAGFTSFVVSQMMMEDILRLGVTLGAGHOKILNS 970
Db 913 DYTFTTTCVGDMLDAIKMGYKFNKFNAGFASFDLVAGMTAEDLLRIGVTLGAGHOKILSS 972

Qy 971 IQWRAQMNQIQSVEV 986
Db 973 IODMRLQMNQTLFVQV 988

RESULT 22
ABU07849

ID ABU07849 standard; protein; 998 AA.

XX AC ABU07849;

XX DT 10-MAY-2003 (first entry)

XX DE Human ephrin receptor ligand EphB3.

XX KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; human;
KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB3.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..33

FT Protein /label= Signal_peptide

FT /label= Mature_EphB3

XX W02003004529-A2.

XX PN 16-JAN-2003.

XX PD 02-JUL-2002; 2002WO-1B002524.

XX PR 02-JUL-2001; 2001US-0302960P.

XX PA (LICN) LICENTIA LTD.

XX PI Alitalo K, Kubo H;

XX DR WPI; 2003-210341/20.

XX DR N-PSDB; ABX12550.

XX Identifying modulators of binding between a Tie receptor tyrosine kinase
XX and an Ephrin ligand, useful for promoting neovascularization, comprises
XX contacting a Tie receptor with an Ephrin in the presence of a putative
XX modulator.

XX Disclosure; Page 142-146; 199pp; English.

XX The invention describes a method of identifying a modulator of binding
XX between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
XX comprises contacting a Tie receptor composition with an Ephrin
XX compound, and detecting the binding between the putative modulator
XX in the presence and in the absence of the putative modulator. The method
XX is useful for identifying a modulator of binding between a Tie receptor
XX tyrosine kinase and an Ephrin ligand. Modulators identified from the
XX method are useful in modulating angiogenic processes, including
XX lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
XX Tie biology, aberrant growth, migration or proliferation of cells that
XX express a Tie receptor, or for promoting growth of vessel or
XX neovascularisation (e.g. ischaemic tissue, an infarction, a new or
XX chronic compound, or a tissue graft or transplant). This is the amino
XX acid sequence of human EphB3, a member of the Ephrin-B subclass of
XX ligands that are bound to the membrane via a transmembrane domain and

cc short cytoplasmic tail and function as Ephrin receptor ligands

XX SO

Sequence 998 AA;

Query Match	70.68;	Score 3661.5;	DB 6;	Length 998;
Best Local Similarity	70.26;	Pred. No. 5.9e-267;		
Matches 692; Conservative 116;	Mismatches 159;	Indels 19;	Gaps 6;	
QY	10	LLLLPL- ----AAVBETLMDSTTAAELGCMVHPSPSGMEEVSGSYDENMNTIRTYQVCN	63	
DB	23	LLLLLLLLPAGCBALBETLMDTKWVTSELAWTSHPSGMEEVSGSYDEAMNPIRTYQVCN	82	
QY	64	VFESSQNNWLRTKFIIRRGAAHRIHVEKMFSDVDCSSIPSPVPGSKCKETFNLYYEADPDSA	123	
DB	83	VRESSQNNWLRTGFIWRDVQVTVVELKFTVRDCNSIPNIPGSKCKETFNLFYFBEADSDVA	142	
QY	124	TKTFPNMNPWVKVDITIADESFQVDLGLGRVMKINTEVRSFGVSRSGFYLAFOQYVG	183	
DB	143	SASSPFWMENPVYKVDITIADESFQVDLGLGRVMKINTEVRSFGVSRSGFYLAFOQYVG	198	
QY	184	CMSLIAVRFYKRCPIRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG	243	
DB	199	CMSLIVRAFYKCCASITAGFALFPETLTGAFTSLVIAPGTCIPNAVEVSPLKLYCNG	258	
QY	244	DGEWLVPFGRCMCKAGFEAVENGTVCRCPGSGTKFANQGDCACTHCPINSTTTSEGAATNC	303	
DB	259	DGEWNVPVGCATCATGHEPFAAKESQCRPPGSGYKAKQGEPCULPCPNSTTTSPAASIC	318	
QY	304	VCRNGYRADLPLDMPCTTIPSPAQOAVISSVNETSLMLEWTPPRDSGGRDLVNIICK	363	
DB	319	TCHNNFYRADSDSDASACTTVPSPRGVINSVNETSLILEWSEPRDLGVRDLDLYNVICK	378	
QY	364	SC--GSGRGACTRCGDNVQYAPRQILGTPRIYISDLLAHTOYTEIQAQNVGVTDOQSPFS	421	
DB	379	KCHGAGGASACSRCDNVFVPRQLGSEPRVHTSHLLAHTRYTTEVOAVNGSVGSPLP	438	
QY	422	POFASVNTTNOAAPSAYSIMHOVSRTVDSITLSWSQDQNGVILDYELOVYKELSEY	481	
DB	439	PRYAAVNTTNOAASEVPTLRLHSSGSLTSLWAPERPNGVILDEMYKFEK--SEG	496	
QY	482	NATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGYGRYSGKMYFOTMTE-ABYQTSIQEK	540	
DB	497	IASTVTSQWNSVQLDGLRPDARYVYVQVRAARTVAGYGRYSGKMYFOTMTE-ABYQTSIQEK	556	
QY	541	LPLITGSSAAGLVFLIAVVIIVNRCRGERADSEYTDKLQHYTSCHMTGCMKLYIDPF	600	
DB	557	LPLIVGSGTAGLVFVVAVVVIAIVCLRKHQHSSEYTEKLQOY---IAPCMKLYIDPF	612	
QY	601	TYEDDNEAVREFAKEDISCVKIEOVIGAGEGEVCSGHLKLPGRKEIPVAIKTLKSGYT	660	
DB	613	TYEDDNEAVREFAKEDISCVKIEEVIGAGEGEVCRGLKLPGRREVFAIKTLKVGYT	672	
QY	661	EKQRDFLSEASIMGQFDHPNVTHLEGVYTKSTPVMITFPMWNSGLDSFLRQNDQOFTV	720	
DB	673	EKQRDFLSEASIMGQFDHPNIIRLEGVYTKSRPVMILTFPMENCALDSFLRLNDQOFTV	732	
QY	721	IOIVGMLRGIAGMKYLADNVYVHRLAARNILVNSNLCKYSDGSLRFEDEDDSDPTY	780	
DB	733	IOIVGMLRGIAGMKYLSNNYVHRLAARNILVNSNLCKYSDGSLRFEDEDDSDPTY	792	
QY	781	TSALGKGIPIRTWAPAIAIYRKFTSASDVMSYGIWNWVMSYGERPYDWTNQDVINAIE	840	
DB	793	TSALGKGIPIRTWAPAIAIYRKFTSASDVMSYGIWNWVMSYGERPYDWTNQDVINAIE	852	
QY	841	QDYRLPPPPWDCPSALHQLMDCWQKQDNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI	900	
DB	853	QDYRLPPPPWDCPTALHQLMDCWVRDNRNLPRKFSQIVNTLDMKIRNAASLKVIASAQSGM	912	
QY	901	NLPLDRTTTPDYTSNTVDWLEAIIKMGQYKESFANAGTFSFDWVSQMMMEDILRLGVTL	960	
DB	913	SQPLLORTTVPDYTIFFTVGDWLDLAIKMGYKESFVSGAFASFDLVAQMTAEDLLRIGVTL	972	
QY	961	AGHQKILNLSIQVMRAQMNQIQSFEV	986	

973 AGHOKKILSSIODMRLOMNQTLPVQV 998

RESULT 23

AD E38343

ID ADE38343 standard; protein; 998 AA.

AC ADE38343;

29-JAN-2004 (first entry)

Human protein 1470 amino acid sequence.

XXIX tumorigenic disorder: angiogenic disorder

KW aberrant protein activity; cytosolic; aminotransferase, and malate dehydrogenase;
 KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
 KW prostatic cancer; Grave's disease; diabetic retinopathy; protein 1470
 XX
 OS Homo sapiens.

PN WO2003065006-A2.

07-AUG-2003

XX
DE
20-JAN-2003. 2003W0-IIS002588.XX
BB
31-JAN-2003. 2002UIS-0353600P.

PR 15-MAR-2002; 2002US-036451/F.

PR 10-APR-2002; 2002US-03/150/P.

PR 19-APR-2002; 2002US-03/4194P.

PR 31-MAY-2002; 2002US-0385023P.

PR 17-JUN-2002; 2002US-0389395P.

PR 15-JUL-2002; 2002US-0395944P.

PR 13-AUG-2002; 2002US-0403046P.

PR 27-AUG-2002; 2002US-0406361P.

PR 12-NOV-2002; 2002US-0425456P.

PR 10-DEC-2002; 2002US-0432122P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Hunter JJ, Macbeth KJ, Tsai

XX
T

DR N-PSDB: ADE38342.

Treating subject having tumor

PT caused by aberrant poly-peptide acid by administering a modu-

XX
PS
Disclosure: SEO ID NO 4: 4541

XX
CC
This invention relates to a

CC having a tumourigenic disorder

modulator. The modulator may have cytostatic, antiproliferative, or antitumoral activity. The method is useful for treating cancer.

cc having a tumour/germ of angiothrombosis
cc having a tumour/germ of angiothrombosis
cc having a tumour/germ of angiothrombosis
cc having a tumour/germ of angiothrombosis
cc having a tumour/germ of angiothrombosis

CC cancer) and, for exa

CC protein 1470 of t

SQ. Sequence 998 AA;

Query Match 70.6%; Score 3661.5; DB 7; Length 998;
Best Local Similarity 70.2%; Pred. No. 5.9e-267;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVETLMDSTTATAGLGMVHPSPSGWEEVSGYDENMTIRTYQVCN 63
Db 23 LLLPLLLPAGCRALBETLMDTKWVTSSELATWSPSGWEEVSGYDENMTIRTYQVCN 82
Qy 64 VFESSQNNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFDSA 123
Db 83 VRESSQNNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFDSA 142
Qy 124 TKTPNNMENPWKVDITIAADESPQVDLGRVNMKINTEVRSFGFVSRSGFYLAFOQYGG 183
Db 143 SASSPFWMENPVYKVDITIADESEFRLDAG----RVNTKVSFGPLSKAGFYLAFOQGA 198
Qy 184 CMSLIARVVRFKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243
Db 199 CMSLISVRAFYKCASTTAGPALPETLTGAEPSTSLVIAQTCIPNAVEVSPVPLKLYCNG 258
Qy 244 DGEWLVDIGRCMKAGFEAVENGTVCRGCPGTGKANOQDEACTHCPINRSTTSEGATNC 303
Db 259 DGEWVVPVGACTCATGHEPAKESQCRPCPGSYKAKQGGPCPLCPNRTTSPAAASIC 318
Qy 304 VCRNGYYRADLDPLDMCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVYNIICK 363
Db 319 TCHNPFYRAGDSADSACTVPSPPRGVINSVNETSLILEWSEPRDLGVRRDLLYNVICK 378
Qy 364 SC--GSGRGACTRCGDNVQAPROGLTEPRIYISDILLAHTQYTFETQAVNGVTDQSPFS 421
Db 379 KCHGAGGASACRDCDDNVFVPRQLGSEPRVHTSHLLAHTRYTFEYQAVNGVSGKSLP 438
Qy 422 PQFASVNTITNOARPSAVSIMHQSRTVDSTLTSWSOPDQPNGLVDLYEQLYKELEY 481
Db 439 PRVAANVNTITNOARPSAVSIMHQSRTVDSTLTSWSOPDQPNGLVDLYEQLYKELEY 496
Qy 482 NATAIKSPNTVTVQGLKAGAIYVQVARTVAGYRGYSGMYPQMTWTE-AYEQTSTQEK 540
Db 497 IASTVTSOMNSVQLDGLRLDARYVQVARTVAGYRGYSGMYPQMTWTE-AYEQTSTQEK 556
Qy 541 LPLIIGSAGLPLIAVVIIVCNRRGFERADSEYTDKLOHTYSGHMTFGMKIYIDPF 600
Db 557 LPLIVGATAGLPLVAVVIAIIVCLRKQRHSGDSEYTEKLOQY----IAPGMKVIIDPF 612
Qy 601 TYEDPNEAVREFAKEIDISCVKIEOVIGAGEFGVCSGHLKLPCKRIIFVAIKTKSGYT 660
Db 613 TYEDPNEAVREFAKEIDISCVKIEOVIGAGEFGVCSGHLKLPCKRIIFVAIKTKSGYT 672
Qy 661 EKQRDFLSEASIMGQFDHPNVIHLEGVTKSTPVMITTEFMENGSLDSFLRQNDGQFTV 720
Db 673 ERQRDFLSEASIMGQFDHPNVIHLEGVTKSTPVMITTEFMENGSLDSFLRQNDGQFTV 732
Qy 721 IQLVGLRGIAAGMKYLAADNMYVHRDLAARNILVNSLVCKVSPDFGLSRLEDDTSDPTY 780
Db 733 IQLVGLRGIAAGMKYLAADNMYVHRDLAARNILVNSLVCKVSPDFGLSRLEDDTSDPTY 792
Qy 781 TSALGGKIPRTWTAPEAIQYKFTSASDVMSYGIWMVMSYGERPYWDMTNDQVINAIE 840
Db 793 TSSLGGKIPRTWTAPEAIQYKFTSASDVMSYGIWMVMSYGERPYWDMTNDQVINAIE 852
Qy 841 QDRLPPLPMDCPSALHQLMDCWOKDRNHRPKFQIVNTLDKMRNNSLKAMAPLSSGI 900
Db 853 QDRLPPLPMDCPSALHQLMDCWOKDRNHRPKFQIVNTLDKMRNNSLKAMAPLSSGI 912
Qy 901 NLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFQVVSQMMEDILRLGVTL 960
Db 913 SQPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFQVVSQMMEDILRLGVTL 972
Qy 961 AGHOKKILNSIQVRAQWQNIQSV 986
Db 973 AGHOKKILNSIQVRAQWQNIQSV 998

RESULT 24
ADD93259

ID ADD93259 standard; protein; 998 AA.

XX ADD93259;

XX 29-JAN-2004 (first entry)

XX CCMP-1.

XX CCMP-1; receptor tyrosine kinase; ephrin B-type receptor 3;
XX prostate cancer; small cell lung carcinoma; peripheral membrane;
XX colorectal cancer; cell membrane; breast cancer; colon cancer.
XX Homo sapiens.

XX Key Location/Qualifiers
XX Peptide 904..919
XX /label= Tandem mass spectrum

XX W02003087841-A2.

XX 23-OCT-2003.

XX 09-APR-2003; 2003WO-GB001593.

XX 09-APR-2002; 2002GB-00008089.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Boyd RS, Fletcher GC, Hudson LJ, Patel S, Terrett JA;

XX MPI; 2003-833798/77.

XX N-PSDB; ADD93260.

XX Screening for or diagnosing carcinoma in a subject or monitoring the
XX effectiveness of carcinoma therapy by detecting and/or quantifying in a
XX biological sample obtained from the subject a CCMP-1 polypeptide or a
XX nucleic acid molecule.

XX Claim 1; Fig 1; 62pp; English.

XX This sequence represents the CCMP-1 protein, which is a receptor tyrosine
XX kinase also known as ephrin B-type receptor 3. CCMP-1 is one of 15 genes
XX overexpressed in prostate cancer tissue, and has also been found at
XX moderate to low levels in three out of four small cell lung carcinoma
XX cell lines. CCMP-1 is localised to the peripheral membrane. It was
XX isolated from colorectal cancer cell membranes and breast cancer cell
XX membranes, purified by 1D gel electrophoresis and characterised by mass
XX spectrometry before being cloned. CCMP-1 may be used in the method of the
XX invention for screening for and/or diagnosing carcinoma in a subject
XX and/or monitoring the effectiveness of carcinoma therapy. The method
XX comprises detecting and/or quantifying in a biological sample obtained
XX from the subject, a CCMP-1 polypeptide or a nucleic acid molecule. The
XX CCMP-1 polypeptide, the nucleic acid molecule, an antibody or agent which
XX interacts with, or modulates the expression or activity of a CCMP-1
XX polypeptide or the expression of a CCMP-1 nucleic acid, is useful in the
XX manufacture of a medicament for treating or preventing carcinoma, e.g.,
XX breast cancer or colon cancer.

XX SQ Sequence 998 AA;

Query Match 70.6%; Score 3661.5; DB 7; Length 998;

Best Local Similarity 70.2%; Pred. No. 5.9e-267;

Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVETLMDSTTATAGLGMVHPSPSGWEEVSGYDENMTIRTYQVCN 63

Db 23 LLLPLLLPAGCRALBETLMDTKWVTSSELATWSPSGWEEVSGYDENMTIRTYQVCN 82

Qy 64 VFESSQNNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFDSA 123

Db 83 VRESSQNNWLTGFIWRDQVVRVVELKFTVRDCNSIPNIPGSKETFNLYEADSDVA 142
 Qy 124 TKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFGPVSRSFYLAFOYGG 183
 Db 143 SASSPFWMENPYKVDITIAPEDESFLDAG---RVNKKVRSFGPLSKAGFYLAFOQGA 198
 Qy 184 CMSLIARVVRKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243
 Db 199 CMSLISVRAFYKCKASTTAGFALPETLTGAETSLVIAFGTCIPNAVEVSVPLKLYCNG 258
 Qy 244 DGEWLVPIGRCMCKAGFEAVENGTVCRGCPGTFKANKQGDCACTHCINRSTTSEGATNC 303
 Db 259 DGEWVPVGACTCATGHEPAKESQCRPCPPGSKAKQGEPCCLPCPPNSRTTSPAASIC 318
 Qy 304 VCRNGYTRADLDPLDMPCTTIPSAQAVISVNNETSLMLEWTPPRDSGGREDLVYNLICK 363
 Db 319 TCHNFYRADSDSADSACTTVPSPRGVSNVNNETSLILEWSEPRDLGVDRDLDLYNVICK 378
 Qy 364 SC--GSGRGACTRCGDNVQVAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPPS 421
 Db 379 KCHGAGGASACSRCDNDNVEFVRQLGLSEPRVHTSHLLAHTRYTFEIQAVNGVSGKSLP 438
 Qy 422 POFASVNTTNOAAPSVAIVMHOVSRVTDSTLWSQDPNGVILDYELQYKEKSEY 481
 Db 439 PRYAAVNTTNOAAPSVEPTLRLHSSGSSLTLSWAPPERNGVILDYEMKYPEK--SEG 496
 Qy 482 NATAIKSGTNTVTVQGLKAGAIYVQVARTVAGYGRYSGMYPTQWTE-AEYQTSIOEK 540
 Db 497 IASTVTSQMSVQLDGLRDPARYVQVARTVAGYGRYSPAEPTTSERGSQAQQLQEQ 556
 Qy 541 LPLIIGSAGLVFLIAVNTAIACNRRGERASEYTDKLOHVTSGHMTPGMKIYIDPF 600
 Db 557 LPLIVGSATAGLVFVAVNTAIACNRRGERASEYTDKLOHVTSGHMTPGMKIYIDPF 612
 Qy 601 TYEDPNEAVREFAKEIDISCVKIBQVIGAGFGFVSCGHLKLPKRBIFVAIKTKSGYT 660
 Db 613 TYEDPNEAVREFAKEIDVSCVIEBIVGAGFGEVCRGLKQPCRREVFVAIKTKVGYT 672
 Qy 661 EKQRDFLSEASIMQDFHPNVIHLEGVYTKSTPVMITTEPMENGLDLSFLRQNDGQTV 720
 Db 673 ERQRDFLSEASIMQDFHPNIIIRLEGVYTKSTPVMITTEPMENGLDLSFLRQNDGQTV 732
 Qy 721 IOLVCMRLGIAAGWKYLAADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSPTY 780
 Db 733 IOLVCMRLGIAAGWKYLAADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSPTY 792
 Qy 781 TSALGGKIPIRWTAPEATQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTQNDVINAIE 840
 Db 793 TSSLGKKIPIRWTAPEATQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTQNDVINAIE 852
 Qy 841 QDYRLPPMDCPALHQLMLDCWKQDRNHRPKFGQIVNTLDKMTNPNLSLKAMAPLSGI 900
 Db 853 QDYRLPPMDCPALHQLMLDCWKQDRNHRPKFGQIVNTLDKMTNPNLSLKAMAPLSGI 912
 Qy 901 NPLLDRTIPDYTSNTDWELEAKMGQYKESFANAGFTSFVYVVSOMMEDILRLGVTL 960
 Db 913 SQPLDLRTPDYTSNTDWELEAKMGQYKESFANAGFTSFVYVVSOMMEDILRLGVTL 972
 Qy 961 AGHQKILNSIQVMRAQNOIQSVEV 986
 Db 973 AGHQKILNSIQVMRAQNOIQSVEV 998

RESULT 25

ADQ20030

ID ADQ20030 standard; protein; 998 AA.

XX AC ADQ20030;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2850.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW Homo sapiens.
 OS WO2004048938-A2.
 XX 10-JUN-2004.
 PD 26-NOV-2003; 2003WO-US038193.
 XX 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 XX Early detection of soft tissue sarcoma comprises determining expression
 of a gene in a first soft tissue sample and a normal soft tissue sample
 and comparing the gene expression, also useful in treating soft tissue
 sarcoma.

Example 2; SEQ ID NO 2850; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma
 which comprises obtaining a first soft tissue sample from an individual
 and a normal soft tissue sample from the same or different individual,
 determining the expression of a gene in both samples and comparing the
 expression of the gene in both soft tissue samples, where a higher level
 of protein expression in the first soft tissue sample indicates the
 presence of soft tissue sarcoma. The method of the invention has
 cytostatic applications and may be useful for detecting soft tissue
 sarcoma, possibly via gene therapy or vaccine production. The nucleic
 acid sequences may be useful in diagnostic and screening applications.
 The current sequence is that of a human soft tissue sarcoma-upregulated
 protein of the invention. The current sequence is not shown within the
 specification per se but was submitted in CD format by the inventor.

Sequence 998 AA;

Query Match 70.6%; Score 3661.5; DB 8; Length 998;
 Best Local Similarity 70.2%; Pred. No. 5.9e-267;
 Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVEETLMDSTTATAGLWNVHPPSGWEEVSGYDENMNTIRTYQVCN 63
 Db 23 LLLPLLLPAGCRALLETLMDTKWVTSGLAWTSHPESGWEEVSGYDENMNTIRTYQVCN 82
 Qy 64 VFESSQNNWLTGFIWRDQVVRVVELKFTVRDCNSIPNIPGSKETFNLYEADSDVA 123
 Db 83 VRESSQNNWLTGFIWRDQVVRVVELKFTVRDCNSIPNIPGSKETFNLYEADSDVA 142
 Qy 124 TKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFGPVSRSFYLAFOYGG 183
 Db 143 SASSPFWMENPYKVDITIAPEDESFLDAG---RVNKKVRSFGPLSKAGFYLAFOQGA 198
 Qy 184 CMSLIARVVRKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243
 Db 199 CMSLISVRAFYKCKASTTAGFALPETLTGAETSLVIAFGTCIPNAVEVSVPLKLYCNG 258
 Qy 244 DGEWLVPIGRCMCKAGFEAVENGTVCRGCPGTFKANKQGDCACTHCINRSTTSEGATNC 303
 Db 259 DGEWVPVGACTCATGHEPAKESQCRPCPPGSKAKQGEPCCLPCPPNSRTTSPAASIC 318
 Qy 304 VCRNGYTRADLDPLDMPCTTIPSAQAVISVNNETSLMLEWTPPRDSGGREDLVYNLICK 363
 Db 319 TCHNFYRADSDSADSACTTVPSPRGVSNVNNETSLILEWSEPRDLGVDRDLDLYNVICK 378
 Qy 364 SC--GSGRGACTRCGDNVQVAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPPS 421
 Db 379 KCHGAGGASACSRCDNDNVEFVRQLGLSEPRVHTSHLLAHTRYTFEIQAVNGVSGKSLP 438

Db 605 TYEDPNEAVREFAKEIDVSCYKIBEVIGAGEFGEVCRGLKQPGRRVFAIKTLKVGYT 664
 Qy 661 EKQRDFLSASIMQGFDPHNPVHLEGVVTKSTPVMIIITFEMENGLSDSLRNDGQFTV 720
 Db 665 ERQRDFLSASIMQGFDPHNPVHLEGVVTKSTPVMIIITFEMENGLSDSLRNDGQFTV 724
 Qy 721 IQLVGLRGIAAGMKYLADNMVYHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPT 780
 Db 725 IQLVGLRGIAAGMKYLSEMMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPT 784
 Qy 781 TSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQVINAE 840
 Db 785 TSSLGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQVINAE 844
 Qy 841 QDYRLPPPMDCPSALHOLMLDCWOKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGI 900
 Db 845 QDYRLPPPMDCPTALHQLMLDCWDRNLRPKFSQIVNTLDKLRNNAASLKVTAASOGM 904
 Qy 901 NLPLDRTIPDYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960
 Db 905 SQPLDRTVPDYTTFTTVGWLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 964
 Qy 961 AGHOKILNSIQVRAQNMNQIQSV 986
 Db 965 AGHOKILNSIQVRAQNMNQIQSV 990

RESULT 28

AAR75843
 ID AAR75843 standard; protein; 993 AA.

XX AAR75843;

DT 25-MAR-2003 (revised)
 DT 24-NOV-1995 (first entry)

XX Protein p140 cDNA from rat skeletal muscle myoblast cell line L6.

XX Protein p140; insulin; tyrosine phosphorylation.

XX Rattus rattus.

XX EF659883-A2.

XX 28-JUN-1995.

XX 24-NOV-1994; 94EP-00118524.

XX 24-NOV-1993; 93JP-00315806.

XX (ONOY) ONO PHARM CO LTD.

XX Tajima H, Kitagawa K, Ohno H;

XX WPI; 1995-226291/30.

PT Isolated protein p140 polypeptide - and treatment of diabetes based on
 PT tyrosine phosphorylation of protein p140.

XX Claim 1; Page 19-23; 42pp; English.

CC A cDNA library was established from rat skeletal myoblast cell line L6.
 CC DNA fragments of approx. 400 bp were recovered and subjected to cloning.
 CC 20 plasmids were sequenced. Sequence data of cDNA fragments were
 CC constructed to the linkage sequences with the DNA programme DNASIS. The
 CC basic sequence protracted in AAQ90972 was hence constructed. From sequence
 CC data of the whole cDNA length, the ORF was determined. The AA sequence
 CC was further translated and the sequence thus established is illustrated
 CC in AAR75843. One of the frames possesses the 2993-bp ORF, that was
 CC approximated to 3000 bp of the whole ORF length of the Eck family. p140
 CC is used for the prevention and treatment of diabetes. Dosage is 10 microg
 CC -1000 mg (p.o.) or 10 microg-100mg (i.v.). (Updated on 25-MAR-2003 to

CC correct PN field.)
 SQ Sequence 993 AA;

Query Match 69.5%; Score 3603.5; DB 2; Length 993;
 Best Local Similarity 68.5%; Pred. No. 1.4e-262;
 Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

Qy 17 AAVEETILMDSTTATA-----ELGMVHPHPPSGWEEVSGYDENNMNTRTY 59
 Db 11 AAARAAEAETNSLSILVRPTSGSRIDSEFVELAWTSHPSGWEVSADEANMPTTY 70
 Qy 60 QVCNVFESSQNNWLRTKFIIRRGARHIVHEKFSVRDCSSIPSPGSKCTFNLYYEAD 119
 Db 71 QVCNVFESSQNNWLRTGFIWRREVQVRVYVVELKFTVRDCNSIPNIPGSKCTFNLYYEAD 130
 Qy 120 FDSATKTFNNMNPVWVVDITIAADRSFSQVDLGGVRVMTKINTEVRSRSGPYSLAFQ 179
 Db 131 SDVASASSPPFMENPVYKVDITIAADRSFSRLDAG----RVNTKVRSGPLSKAGFYLAQ 186
 Qy 180 DYGGCKSLIAVRVYRKCPRIIQNGAIFQETLSCAESTSLVAARGSCIANAEVDVPIKL 239
 Db 187 DQACNSLSIVRAFYKCASTTAGFALFPETLGAETSLVIAPTCIANA VESVPLKL 246
 Qy 240 YCNGDGEWLVPICRCMKAGFEAVENGTVCRGCPSTGTFKANQOGEACTHCPIINSRTTSEG 299
 Db 247 YCNGDGEWVVPVGACTCATGHEPAAKETQCRACPPGSGYKAKQGEPCPCPPNSRTTSPA 306
 Qy 300 ATNCVCENGYYRADLDPLDMPCTTIPSAPOAVISSVNETSMLMTEWTPRSGREDLVYN 359
 Db 307 ASICTCHNNFYRADSDTADSACTTVPFPPRGVSNVNETSLILEWSEPRDLGRDLDLYN 366
 Qy 360 IICKSGSGRGA-----CTRCGNVOYAPROLGLTEPRIYISDLAHTQVTFEIQAVNGV 414
 Db 367 VICCKRGSGAGGPATCSRCDNVEFEPRLGLTERVHSHLLAHTRTTFEVOAVNGV 426
 Qy 415 TDQSPSPQFASVNTTNQAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELOYY 474
 Db 427 SGKSPLPYAAVNITTNQAAPSEVPTLHLSSGSSSLTSLSWAPPERNGVILDYEMKYF 486
 Qy 475 EKELSEYNATAIKSPNTVTVOGLKAGAIYVFOVRRARTVAGYGRYSKMYFOIWMTE-AEY 533
 Db 487 EK--SKGIASVTVSQKNSVQLDGLQPDARYVVOVRRARTVAGYGRYSKMYFOIWMTE-AEY 544
 Qy 534 QTSIQEKLPLIIIGSSAAGLVFLIAVVVIAIVCNRRGPERADSEYTDKLOHYTSGHMTPCM 593
 Db 545 AQQQLQQLPLIVGSTVAGFVFWVVVIALVCLRKORQGPDAEYTEKLOQY----VAPRM 600
 Qy 594 KIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRREIFVAIK 653
 Db 601 KVIIDPFTYEDPNEAVREFAKEIDVSCVKEIEVIGAGEFGEVCSGHLKLPGRREIFVAIK 660
 Qy 654 TLKSGYTEKORRDFLSEASIMQGFDPHNPVHLEGVVTKSTPVMIIITFEMENGLSDSLRQ 713
 Db 661 TLKVGYTEKORRDFLSEASIMQGFDPHNPVHLEGVVTKSTPVMIIITFEMENGLSDSLRQ 720
 Qy 714 NDCQFTVQLVGLMRLGIAAGMKYLDAMNYYVHRDLAARNILVNSLVCKVDFGLSRFLED 773
 Db 721 NDCQFTVQLVGLMRLGIAAGMKYLDAMNYYVHRDLAARNILVNSLVCKVDFGLSRFLED 780
 Qy 774 DTSDPPTYTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQ 833
 Db 781 DSDPTYTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQ 840
 Qy 834 DVINAIEDYRLPDPMDPSALHOLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNLSKAM 893
 Db 841 DVINAIEDYRLPDPMDPSALHOLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNLSKAM 900
 Qy 894 APLSSGGINPLDRTTIPDYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDI 953
 Db 901 ASAPSGSQPLDRTTIPDYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDI 960
 Qy 954 LRLGVTLAGHOKILNSIQVRAQNMNQIQSV 986

Db	961	LRIGVTLAGHQKILSSIQDMRLQNMOTLPVQV	993
Db	307	ASICTCHNNFYRADSDTADSACTTVPSPRGVSNVNETSLILEWSEPRDLGRRDLYN	366
Qy	360	IICKSCSGRGA-----CTRCGDNVQYAPROGLGTEPIRIYISDLLAHTOYTFEIQAVNGV	414
Db	367	VICKXCRGSGGAGPATCSCDDNVEFEPQULGTERRVHSHLLAHTRYTFEIQAVNGV	426
Qy	415	TDQSPFSPQFASVNITTNQAAPSIVSINHQSRTVDSITLSWSQDPQNGVILDELOYY	474
Db	427	SKGSLPFPYAAVNITTNQAAPSEVPTLHLHSSSGSLTLSWAPERNGVILDEMYKF	486
Qy	475	EKELSEYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYQTWTE-AYE	533
Db	487	ER--SKGIASVTOKNSVQLDGLQPDARYVVOVARTVAGYGRYSPAEFETTSERSSG	544
Qy	534	QTSIOEKPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKIQHTYTSGHMTFGM	593
Db	545	AQOLQQLPLIVGSTVAGFVFWVVVVVIALVCLRKORQGPDAEYTEKLOYY-----VAPRM	600
Qy	594	KIYIDPFTYEDPNEAVREFAKEIDISCVKIBOVIGAGFGEVCSGHLKLPGRKREIFVAIK	653
Db	601	KVIDPFTYEDPNEAVREFAKEIDISCVKIBEVIGAGFGEVCSGHLKLPGRREYFVAIK	660
Qy	654	TLKSGYTEKORRDFLSEASIMQFDPHNVHLLEGVVTKSTPMIITEFMENGLSDSFLRQ	713
Db	661	TLKVGYTEKORRDFLSEASIMQFDPHNIIRLEGVVTKSRPVMILITEFMENCALDSFLRL	720
Qy	714	NDGQFTVIQVLGMLRGIAAGMKYLADMNYYVHRDLAARNILVNSNLVCKVSDPGLSRFLED	773
Db	721	NDGQFTVIQVLGMLRGIAAGMKYLSEMNYYVHRDLAARNILVNSNLVCKVSDPGLSRFLED	780
Qy	774	DTSDPYTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMNQ	833
Db	781	DPSDPYTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMNQ	840
Qy	834	DVNATEQDYRLPPPMDCPSALHQLMDCWKDRNHRPKFGIIVNTLDMKIRNPNSLKAM	893
Db	841	DVNAVEQDYRLPPPMDCPSALHQLMDCWKDRNHRPKFGIIVNTLDMKIRNNSLKVI	900
Qy	894	APLSSGINPLDRTIPTYSFNTVDLEAIKMGQYKESFANAGFTSPDVVSQMMEDI	953
Db	901	ASAPSCMSQPLLDRTVPDVTFTTVDGLDIAIKMGYKESFVAGFAGFASPDVLAQMTAEDL	960
Qy	954	LRIGVTLAGHQKILSSIQDMRLQNMOTLPVQV	993
Db	961	LRIGVTLAGHQKILSSIQDMRLQNMOTLPVQV	993
RESULT 30			
ADU71136	ADU71136 standard; protein; 896 AA.		
XX	ADU71136;		
AC	ADU71136;		
DT	06-MAY-2004 (first entry)		
XX	Human heat mitochondrial protein as a therapeutic target SeqID2942.		
DE	mitochondrial; human; screening assay; diabetes mellitus;		
XX	Huntington's disease; osteoarthritis;		
KW	Leber's hereditary optic neuropathy; LHON;		
KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;		
KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;		
KW	neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;		
KW	osteopathic; ophthalmological; cytostatic.		
OS	Homo sapiens.		
XX	WO2003087768-A2.		
PN	23-OCT-2003.		
PD	04-APR-2003; 2003WO-US010870.		
XX			
PF			

Query Match

Best Local Similarity

Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

17

AAVETLMDSTATA-----ELCMVHPSPGWEVSGVDENNTIRTY

59

11

AAAEERAAAEATNSILVRPTSEGRIDSEFVELAWTSHPSGWEVEVAYDEAMNPIRTY

70

60

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

119

71

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

130

120

FDSATKTFNNMENNPKVDDTTAEDSPQVDLGRVMKINTEVRSFGVRSGLYLAQ

179

131

SDVASASSPFMMENPVYKVTDTIAPDESFSRLDAG----RVNTKVRSGFLSKAGYLAQ

186

180

DYGGCWSLAVFVRKCPRIIQNGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKL

239

187

DQACMSLISVRAFYKCASTAGTALFPETITLGTSLVIAPTCIANAVEVSVPKL

246

240

YNGDGEWLVPICRCMKAGFAVENGVRCPCSGTFFKANGQDEACTHCIPNSITTSSE

299

247

YNGDGEWVVPVGCATCTCATGHEPAKETQCRACPPGSKAKQKQEGFCLPCPPNSRTTSPA

306

300

ATNCVCRNGYYRADLDFLMDPCTTIPSAQVAIVSSVNETSLMLEWTTPPRDSGREDLYN

359

Query Match

Best Local Similarity

Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

17

AAVETLMDSTATA-----ELCMVHPSPGWEVSGVDENNTIRTY

59

11

AAAEERAAAEATNSILVRPTSEGRIDSEFVELAWTSHPSGWEVEVAYDEAMNPIRTY

70

60

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

119

71

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

130

120

FDSATKTFNNMENNPKVDDTTAEDSPQVDLGRVMKINTEVRSFGVRSGLYLAQ

179

131

SDVASASSPFMMENPVYKVTDTIAPDESFSRLDAG----RVNTKVRSGFLSKAGYLAQ

186

180

DYGGCWSLAVFVRKCPRIIQNGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKL

239

187

DQACMSLISVRAFYKCASTAGTALFPETITLGTSLVIAPTCIANAVEVSVPKL

246

240

YNGDGEWLVPICRCMKAGFAVENGVRCPCSGTFFKANGQDEACTHCIPNSITTSSE

299

247

YNGDGEWVVPVGCATCTCATGHEPAKETQCRACPPGSKAKQKQEGFCLPCPPNSRTTSPA

306

300

ATNCVCRNGYYRADLDFLMDPCTTIPSAQVAIVSSVNETSLMLEWTTPPRDSGREDLYN

359

Query Match

Best Local Similarity

Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

17

AAVETLMDSTATA-----ELCMVHPSPGWEVSGVDENNTIRTY

59

11

AAAEERAAAEATNSILVRPTSEGRIDSEFVELAWTSHPSGWEVEVAYDEAMNPIRTY

70

60

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

119

71

QVCNVFESSQNNWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYYEAD

130

120

FDSATKTFNNMENNPKVDDTTAEDSPQVDLGRVMKINTEVRSFGVRSGLYLAQ

179

131

SDVASASSPFMMENPVYKVTDTIAPDESFSRLDAG----RVNTKVRSGFLSKAGYLAQ

186

180

DYGGCWSLAVFVRKCPRIIQNGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKL

239

187

DQACMSLISVRAFYKCASTAGTALFPETITLGTSLVIAPTCIANAVEVSVPKL

246

240

YNGDGEWLVPICRCMKAGFAVENGVRCPCSGTFFKANGQDEACTHCIPNSITTSSE

299

247

YNGDGEWVVPVGCATCTCATGHEPAKETQCRACPPGSKAKQKQEGFCLPCPPNSRTTSPA

306

300

ATNCVCRNGYYRADLDFLMDPCTTIPSAQVAIVSSVNETSLMLEWTTPPRDSGREDLYN

359

Isolated protein p140 polypeptide - and treatment of diabetes based on tyrosine phosphorylation of protein p140.

Example; Page 28-33; 42pp; English.

AAQ0982 does not appear to be referred to in the spec. although it is listed in the sequence listings (SEQ ID No. 4). It is the same length as SEQ ID No. 3 and may be identical to it (see AAQ0982). AAR75822 is the corresp. AA sequence to AAQ0982. It is not referred to in the spec. and may be identical to SEQ ID No. 1 (see AAR75843). (Updated on 25-MAR-2003 to correct PN field.)

Sequence 993 AA;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 16:40:40 ; Search time 48 Seconds
(without alignments)
1976.453 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRRILGAALLLLPLAAVE.....ILNSIQVMRAQMNIQSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5089	98.1	970	2 178842	receptor protein-t
2	4933.5	96.3	995	2 A56599	embryo kinase 5 -
3	3934.5	75.8	984	2 A39753	protein-tyrosine k
4	3767	72.6	985	2 I51672	receptor tyrosine
5	3724	71.8	952	2 I50612	protein-tyrosine k
6	3662.5	70.6	988	2 I50611	protein-tyrosine k
7	3661.5	70.6	998	2 S37627	protein-tyrosine k
8	3630.5	70.0	993	2 I48653	mouse developmen
9	3441	66.3	938	2 I49071	protein kinase - m
10	3075.5	59.3	985	2 I51549	receptor tyrosine
11	3053	58.8	991	2 I78843	receptor protein-t
12	3045	58.7	986	2 I78844	receptor protein-t
13	3040	58.6	986	2 S78059	protein-tyrosine k
14	3028	58.4	998	2 I58351	receptor protein-t
15	3013	58.1	998	2 JC5672	receptor tyrosine
16	3009	58.0	1013	2 I50615	receptor-type prot
17	2939	56.6	981	2 S51604	receptor-like tyro
18	2931	56.5	983	2 B45583	receptor tyrosine
19	2930.5	56.5	983	2 A38224	protein-tyrosine k
20	2923	56.3	1005	2 S49015	receptor tyrosine
21	2897.5	55.7	983	2 A45583	receptor tyrosine
22	2854.5	55.0	987	2 I48652	mouse developmen
23	2844	54.8	987	2 A54092	protein-tyrosine k
24	2811.5	54.2	987	2 I48953	eph-related recept
25	2728.5	52.6	849	2 I50617	protein-tyrosine k
26	2599.5	50.1	948	2 S51605	receptor-like tyro
27	2531	48.8	898	2 S47489	receptor tyrosine
28	2512	48.4	893	2 S51603	receptor-like tyro
29	2476	47.7	478	2 A57174	protein-tyrosine k

30	2471.5	47.6	480	2 I48760	protein-tyrosine k
31	2464	47.5	877	2 I48967	kinase-specific kin
32	2461	47.4	1006	2 JC5526	kinase-defective E
33	2357	45.4	977	2 S49004	tyrosine kinase Mp
34	2356.5	45.4	976	2 A36355	protein-tyrosine k
35	2277	43.9	975	2 I48974	receptor-tyrosine k
36	2259	43.5	612	2 S33506	protein-tyrosine k
37	1933.5	37.3	1019	2 T13039	tyrosine kinase re
38	1862.5	35.9	984	1 A34076	protein-tyrosine k
39	1549	29.9	490	2 I50613	protein-tyrosine k
40	1482.5	28.6	605	2 JC5673	receptor tyrosine
41	1475	28.4	610	2 I48612	developmental kina
42	1472.5	28.4	626	2 I48614	developmental kina
43	1432	27.6	1122	2 T42400	Eph receptor tyros
44	1332	25.7	426	2 I48759	protein-tyrosine k
45	1257.5	24.2	919	2 T29581	hypothetical prote
46	1211	23.3	275	2 I48761	protein-tyrosine k
47	1204.5	23.2	372	2 S23363	protein-tyrosine k
48	771.5	14.9	334	2 T43450	hypothetical prote
49	636	12.3	505	1 S24550	protein-tyrosine k
50	631.5	12.2	506	1 S24553	protein-tyrosine k
51	612	11.8	1300	2 A36502	insulin receptor-r
52	611	11.8	1367	1 IGHUR1	insulin-like growt
53	606.5	11.7	507	1 A39339	protein-tyrosine k
54	605.5	11.7	541	2 S31645	protein-tyrosine k
55	604	11.6	1383	2 A36080	insulin receptor p
56	603	11.6	1372	2 A34157	insulin receptor p
57	600	11.6	512	1 I56160	protein-tyrosine k
58	600	11.6	1382	1 INHUR	insulin receptor p
59	599.5	11.6	1371	2 A33837	insulin-like growt
60	599.5	11.6	1520	1 TVFPA	protein-tyrosine k
61	594.5	11.5	505	1 TVHUHC	protein-tyrosine k
62	594	11.4	509	1 I48845	protein-tyrosine k
63	594	11.4	542	2 A49114	protein-tyrosine k
64	592	11.4	512	1 A39719	protein-tyrosine k
65	591.5	11.4	512	1 TVHULY	protein-tyrosine k
66	591	11.4	1134	1 JN0711	protein-tyrosine k
67	590.5	11.4	528	1 TVFVG9	protein-tyrosine k
68	590.5	11.4	2338	2 I73957	kinase-related pro
69	589.5	11.4	543	1 TVHUY5	protein-tyrosine k
70	588.5	11.3	541	1 TVCHYS	protein-tyrosine k
71	588	11.3	509	1 OKHULK	protein-tyrosine k
72	587.5	11.3	1363	2 T43220	insulin-like growt
73	587	11.3	1268	2 B36502	insulin receptor-r
74	586.5	11.3	1136	1 S57845	protein-tyrosine k
75	585	11.3	536	2 S33569	protein-tyrosine k
76	584	11.3	537	2 I51592	protein-tyrosine k
77	583.5	11.2	537	1 A45501	protein-tyrosine k
78	583.5	11.2	803	1 OKFFPS	protein-tyrosine k
79	583	11.2	532	1 A34104	protein-tyrosine k
80	583	11.2	532	1 B34104	protein-tyrosine k
81	582.5	11.2	539	2 B49114	protein-tyrosine k
82	582	11.2	496	2 T22405	protein-tyrosine k
83	581.5	11.2	503	1 TVMSHC	protein-tyrosine k
84	580.5	11.2	334	2 S24552	protein-tyrosine k
85	580	11.2	534	1 S33568	protein-tyrosine k
86	579.5	11.2	503	1 JQ1321	protein-tyrosine k
87	579.5	11.2	2340	2 I48310	kinase-related pro
88	579	11.2	512	2 I49552	protein-tyrosine k
89	579	11.2	534	1 A44991	protein-tyrosine k
90	579	11.2	587	1 TVFVPR	protein-tyrosine k
91	578.5	11.2	533	1 TVCHUS	protein-tyrosine k
92	578.5	11.2	537	1 TVHUY5	protein-tyrosine k
93	578.5	11.2	544	2 I51593	protein-tyrosine k
94	578.5	11.2	557	1 TVFVS2	protein-tyrosine k
95	578.5	11.2	568	1 TVFVS1	protein-tyrosine k
96	577.5	11.1	526	2 S15582	protein-tyrosine k
97	577	11.1	526	2 S26420	protein-tyrosine k
98	577	11.1	640	2 S23008	insulin-like growt
99	577	11.1	1052	2 I53012	focal adhesion kin
100	576	11.1	981	1 FOMVGM	gag-abl polyprotei

ALIGNMENTS

RESULT 1
I78842
receptor protein-tyrosine kinase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C;Accession: I78842
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty A;Reference number: I58351; MUID:95206782; PMID:7898931
A;Accession: I78842
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-970 <RES>
A;Cross-references: GB:L36643; NID:g551609; PID:AAA74244.1; PID:g551610
C;Genetics:
A;Gene: HEK5
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h F;603-871/Domain: protein kinase homology <Kin>
F;894-960/Domain: SAM homology <SAM>

Query Match 98.1%; Score 5089; DB 2; Length 970;
Best Local Similarity 99.4%; Pred. No. 2.7e-225;
Matches 966; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 15 LLAVESTLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 74
Db 1 LLAVESTLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 60

Qy 75 TKFIRRGARHIVHEMFVSRDCCSIPSPGCKETENLYVYADPDSATKTPNNMENP 134
Db 61 TKFIRRGARHIVHEMFVSRDCCSIPSPGCKETENLYVYADPDSATKTPNNMENP 120

Qy 135 WKVVDTTAADESFSQVDLGRVVKINTEVRSFGVSRGFLAFQDYGGCWSLIAVRVY 194
Db 121 WKVVDTTAADESFSQVDLGRVVKINTEVRSFGVSRGFLAFQDYGGCWSLIAVRVY 180

Qy 195 RKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 254
Db 181 RKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240

Qy 255 MCKAGFEAVNGTVCRCPSTGFRKANGDEACTHCPINSTRRTSEGATNCVCRNGYRADL 314
Db 241 MCKAGFEAVNGTVCRCPSTGFRKANGDEACTHCPINSTRRTSEGATNCVCRNGYRADL 300

Qy 315 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 374
Db 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360

Qy 375 CGDNVQVAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQASVNIITNQA 434
Db 361 CGDNVQVAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQASVNIITNQA 420

Qy 435 APSAVSTMHQSRTVDSTILSWSPDQPNGLVDYELQYKEKSEYNATAIKSPNTVT 494
Db 421 APSAVSTMHQSRTVDSTILSWSPDQPNGLVDYELQYKEKSEYNATAIKSPNTVT 480

Qy 495 VQGLKAGAIYVQVRAARTVAGYGRYSGMYFQTMTEAEYQTSIQEKLPLIIGSSAAGLVF 554
Db 481 --GLKAGAIYVQVRAARTVAGYGRYSGMYFQTMTEAEYQTSIQEKLPLIIGSSAAGLVF 538

Qy 555 LIAVWVIAVCNRRGFPRASEYTDKLOHTYSGHMTFGMKIYIDPFTYEDPNEAVREFAK 614
Db 539 LIAVWVIAVCNRRGFPRASEYTDKLOHTYSGHMTFGMKIYIDPFTYEDPNEAVREFAK 598

Qy 615 EIDIISCVKIEQVIGAGFGEVCSHLKLPKGRFELFAIKTLKSYTEKQRDRDPLSEASIM 674
Db 599 EIDIISCVKIEQVIGAGFGEVCSHLKLPKGRFELFAIKTLKSYTEKQRDRDPLSEASIM 658

Qy 675 GQFDHPNVIHLEGVVTKSTPVMIIITFPMENGLSDSLRQNDGQFTVIQLVGLMRLGIAAGM 734

Db 659 GQFDHPNVIHLEGVVTKSTPVMIIITFPMENGLSDSLRQNDGQFTVIQLVGLMRLGIAAGM 718
Qy 735 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGGKIPIRWTA 794
Db 719 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGGKIPIRWTA 778
Qy 795 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPVDWMTNODVINAIQDYLRLPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPVDWMTNODVINAIQDYLRLPPMDCPSA 838
Qy 855 LHQLMLDCWQKDRNHRPKFGQIVNTLDMKMRNPSLKAMAPLSSGINLPLDRTIIPDYS 914
Db 839 LHQLMLDCWQKDRNHRPKFGQIVNTLDMKMRNPSLKAMAPLSSGINLPLDRTIIPDYS 898
Qy 915 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSOMMEDILRLGVTLAGHOKKILNSIQVM 974
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSOMMEDILRLGVTLAGHOKKILNSIQVM 958
Qy 975 RAQMNOIQSVEV 986
Db 959 RAQMNOIQSVEV 970

RESULT 2
A56599
embryo kinase 5 - chicken
N;Alternate names: receptor tyrosine kinase Cek5
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Gallus gallus (chicken)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
C;Accession: A56599
R;Pasquale, E.B.
Cell Regul. 2, 523-534, 1991
A;Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor. A;Reference number: A56599; MUID:92144672; PMID:1664238
A;Accession: A56599
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-995 <PAS>
A;Cross-references: GB:M62325; NID:g211448; PID:AAA48667.1; PID:g211449
A;Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBI:P:82001)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin F;628-896/Domain: protein kinase homology <Kin>
F;636-644/Region: protein kinase ATP-binding motif
F;919-985/Domain: SAM homology <SAM>

Query Match 96.3%; Score 4993.5; DB 2; Length 995;
Best Local Similarity 95.8%; Pred. No. 6.5e-221;
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

Qy 10 LLLPLLAEEFTLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQ 69
Db 18 LALLPLAAVEETLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQ 77

Qy 70 NNWLRTKTRRRCGARHIVHEMFVSRDCCSIPSPGCKETENLYVYADPDSATKTFPN 129
Db 78 NNWLRTKTRRRCGARHIVHEMFVSRDCCSIPSPGCKETENLYVYADPDSATKTFPN 137

Qy 130 WMENPMVKVDITIAADESFSQVDLGRVVKINTEVRSFGVSRGFLAFQDYGGCWSLIA 189
Db 138 WMENPMVKVDITIAADESFSQVDLGRVVKINTEVRSFGVSRGFLAFQDYGGCWSLIA 197

Qy 190 VRVYRKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV 249
Db 198 VRVYRKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLV 257

Qy 250 PIGRCMCKAGFEAVNGTVCRCPSTGFRKANGDEACTHCPINSTRRTSEGATNCVCRNGY 309
Db 258 PIGRCMCKAGFEAVNGTVCRCPSTGFRKANGDEACTHCPINSTRRTSEGATNCVCRNGY 317

Qy 310 YRADLPDLMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369

Db 318 YRADADPDMPTTIPSAQAVISVNETSLMELTTPRDSGGREDIVYNIICKSCSGR 377
Qy 370 GACTRCGDNVQYAPROGLGLEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 429
Db 378 GACTRCGDNVQYAPROGLGLEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 437
Qy 430 TTNOAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 489
Db 438 TTNOAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKSELNSTAVKSP 497
Qy 490 TMTVVOGLKAGAIYVQVQVARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSA 549
Db 498 TMTVVOGLKAGAIYVQVQVARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSA 557
Qy 550 AGLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEA 608
Db 558 AGLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEA 617
Qy 609 VREPAKEIDISCVKIEQVIGAGEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 668
Db 618 VREPAKEIDISCVKIEQVIGAGEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 677
Qy 669 SEASIMQFDPHPNVIHLEGVVTKSTPVMITPEFMENGLSDSFLRQNDGQFTVIOLVGMLR 728
Db 678 SEASIMQFDPHPNVIHLEGVVTKSTPVMITPEFMENGLSDSFLRQNDGQFTVIOLVGMLR 737
Qy 729 GIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLEDDTSDPTYSALGSKI 788
Db 738 GIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLEDDTSDPTYSALGSKI 797
Qy 789 PIWTAPEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYDMTNDQVINAIEQDYRLPPP 848
Db 798 PIWTAPEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYDMTNDQVINAIEQDYRLPPP 857
Qy 849 MDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIKRNPNLSKAMAPLSSGINPLLDRT 908
Db 858 MDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIKRNPNLSKAMAPLSSGINPLLDRT 917
Qy 909 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKIL 968
Db 918 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKIL 977
Qy 969 NSIQVMEARQNMQIQSVEV 986
Db 978 NSIQVMEARQNMQIQSVEV 995

RESULT 3

A39753
protein-tyrosine kinase (EC 2.7.1.112) elk precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A39753; S04327
R:Lhotak, V.; Greer, P.; Letwin, K.; Pawson, T.
Mol. Cell. Biol. 11, 2496-2502, 1991
A:Title: Characterization of elk, a brain-specific receptor tyrosine kinase.
A:Reference number: A39753; PMID:91203869; PMID:2017163
A:Accession: A39753
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-984 <LHO>
A:Cross-references: UNIPROT:P09759; GB:M59814
R:Letwin, K.; Yee, S.P.; Pawson, T.
Oncogene 3, 621-627, 1988
A:Title: Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned using anti-tyrosine kinase antibody.
A:Reference number: S04327; MUID:94167102; PMID:2485255
A:Accession: S04327
A:Molecule type: mRNA
A:Residues: 605-984 <LET>
A:Cross-references: EMBL:X13411; NID:g56094; PIDN:CAA31777.1; PID:g56095
C:Genetics:
A:Gene: elk

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat he
C:Keywords: ATP; autophosphorylation; kinase-related transforming protein; phosphoprotein
F:617-885/Domain: protein kinase homology <KIN>
F:625-633/Region: protein kinase ATP-binding motif
F:908-974/Domain: SAM homology <SAM>

Query Match 75.8%; Score 3934.5; DB 2; Length 984;
Best Local Similarity 73.9%; Pred. No. 1.5e-172;
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;
Qy 11 LLLPLLAAREETLMDSTTATAELGMMVHPSPSGVEEVSVDENMTITQYQCNVFESSQ 70
Db 10 LLASAAAMEETLMDTARTATAELGMMVHPSPSGVEEVSVDENMTITQYQCNVFESSQ 69
Qy 71 NWLRTFPIRRGAHRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEADTSATKTFPNW 130
Db 70 NWLRTFPIRRGAHRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEADTSATKTFPNW 129
Qy 131 MENPWKVDITAADESPQVDLGGVRVMKINTEVRSPGVSRSFYLAQDYGCGMSLIIV 190
Db 130 SEAPYLKVDITAADESPQVDLGGVRVMKINTEVRSPGVSRSFYLAQDYGCGMSLIIV 189
Qy 191 RVFTRKCPRIIONGAIFQETLSGABSTSLVAARSGCIANAEEVDVPIKLYCNGDGEWLP 250
Db 190 RVFTRKCPRIIONGAIFQETLSGABSTSLVAARSGCIANAEEVDVPIKLYCNGDGEWLP 249
Qy 251 IGRCMKAGPEAVENGTVCRGCPSTFKANQGEACTHCPINSGRTTSEGATNCVCRNGY 310
Db 250 IGRCTCKAGYEP-ENSVAACKACAGTFKASQEAEGSCHSPNSRSPSEASPICTCRGY 308
Qy 311 RADLDPLDMPCTTIPSAQAVISVNETSLMELTTPRDSGGREDIVYNIICKSCSGRG 370
Db 309 RADFDPEVACTSPVSGPRNVISIVNETSIILEMHPRETGRDQDVYNIICKCRADR 368
Qy 371 ACTRCGDNVQYAPROGLGLEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 430
Db 369 SCRCDDNVFVRPQGLTECRVISLSLWHTPTFDIQAINGVSSKSPPPQHVSNIT 428
Qy 431 TNOAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 490
Db 429 TNOAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 488
Qy 491 NTVTVOGLKAGAIYVQVQVARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSA 550
Db 489 NTARIDGLRPGMVVQVQVARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSA 548
Qy 551 GLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEAVR 610
Db 549 GVVFVWSLVSAISIVCSKRAYSKYAVSDKLOHYSTGRGSPGMKIYIDPFTVEDPNEAVR 608
Qy 611 EFAKEIDISCVKIEQVIGAGEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLSE 670
Db 609 EFAKEIDISCVKIEQVIGAGEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLSE 668
Qy 671 ASIMQFDPHPNVIHLEGVVTKSTPVMITPEFMENGLSDSFLRQNDGQFTVIOLVGMLR 730
Db 669 ASIMQFDPHPNVIHLEGVVTKSTPVMITPEFMENGLSDSFLRQNDGQFTVIOLVGMLR 728
Qy 731 AAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLEDDTSDPTYSALGSKI 790
Db 729 AAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLEDDTSDPTYSALGSKI 788
Qy 791 RWTAPAEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYDMTNDQVINAIEQDYRLPPP 850
Db 789 RWTAPAEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYDMTNDQVINAIEQDYRLPPP 848
Qy 851 CPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIKRNPNLSKAMAPLSSGINPLLDRTIP 910
Db 849 CPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIKRNPNLSKAMAPLSSGINPLLDRTIP 908
Qy 911 DYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKILNS 970
Db 909 DYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKILNS 968

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Qy 971 IQWRAQMNIQSV 984
Db 969 IHSMRVQMNSPSV 982

RESULT 4
151672
receptor tyrosine kinase - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51672
C:Jones, T.L.; Karavanova, I.; Maeno, M.; Ong, R.C.; Kung, H.F.; Daar, I.O.
Oncogene 10, 1111-1117, 1995
A:Title: Expression of an amphibian homolog of the Eph family of receptor tyrosine kinase
A:Reference number: I51672; MUID:95215070; PMID:7700636
A:Accession: I51672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-985 <JON>
A:Cross-references: UNIPROT:Q91571; EMBL:U14164; NID:9557214; PIDN:AAA74888.1; PID:99572
C:Genetics:
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:618-886/Domain: protein kinase homology <KIN>
F:626-634/Region: protein kinase ATP-binding motif
F:909-975/Domain: SAM homology <SAM>

Query Match 72.6%; Score 3767; DB 2; Length 985;
Best Local Similarity 71.2%; Pred. No. 6.6e-165;
Matches 699; Conservative 131; Mismatches 140; Indels 12; Gaps 5;

Qy 6 LGALLLLPL-----LAAVEETLMDSTTATAELGWMVHPSPGSEVSGYDENMTIRYQV 61
Db 3 LNVLLLLCLSGGQVGAEEETMDTRTATALGWTANPPSGGEEVSGYDENMTIRYQV 62

Qy 62 CNVFESSONNWLRTKFIIRRGARHIVHEMKFSVRDCSSIPSPGSCKETFNLYYYEADFD 121
Db 63 CNVFGPKQNNWLLTFIPRGARHIVYEMRTVRDCSSLPNVPSCKETFNLYYYEADSN 122

Qy 122 SATKTFPNNMNPVVKDTTAADESFQVDLGGRVKINTEVRSFGVSRSGFLAFQDY 181
Db 123 IENKISTFWNESPLVKDVTAADESFQVDLGGRVKINTEVRSFGFLTRSGFLAFQDY 182

Qy 182 GCKSLIAVRVYRKCPIRIQNGALFOETLGAESTSLVAARGSCIANAEVDVPIKLYC 241
Db 183 GACMELLSVRVFFKEMPSVQVQLLVFPTMTGAESTSLVIARGTCIPNAEEVDVPIKLYC 242

Qy 242 NGDGEWLVPIGRCMKAGFEAVENGTVCRGCPGSGTFFKANQGDGDEACTHCPINSRTTSEGAT 301
Db 243 NGDGEWVVPIGKCTCKAGVEP-ENHVCKACPAAMFKANQGMGICACQCPANSRSTSEASP 301

Qy 302 NCVCRNGYRADLPLDMPCTTIPAPQAVTSSVNETSLMLEWPPRDSGGREDLVNII 361
Db 302 ICICRNGYRADFDTPAECTSVPSGPRNVIISVNETAITLEWPPRPTGRDQVDVNIIV 361

Qy 362 CKSCGSGRGACRCGDNVQYAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFS 421
Db 362 CKKCRADRCRCDNDVDFVROLGLDTRVFIISNLWAHTPYTFETQAVNGVINKSPFP 421

Qy 422 PQFASVNIITNQAAPSIVSMHQVSRVDSITLWSQPDQPNQGVILDELOYYEKEISEY 481
Db 422 PQHVSNIITNQAAPSIVSMHQVSRVDSITLWSQPDQPNQGVILDELOYYEKEISEY 481

Qy 482 NATATKSPNTTVVQGLKAGALYVF---QVRARTVAGYGRYSGKMYFOTMTAEAYQTSIQ 538
Db 482 NSSLSARSONTARTG---GRRVFMVSVQVARTVAGYGRYSGKMYFOTMTAEAYQTSIQ 538

Qy 539 EKPLPIIGSAAAGLVIAVAVIAVCNRRRGERADSEYTKLQHYTSGHWTGPKMKIYID 598
Db 539 EQPLPL-TGSAAGVGVFVLSVAISIVCSRKRTYSKEAVYSDKLQHYSTGRSGPGMKIYID 597
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Qy 599 PFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSHLKLPGRKEIFVAIKTLKSG 658
Db 598 PFTYEDPNEAVREFAKEIDVSVFKIEEVIGAGEFGEVYKGRKLPGRKEISVAIKTLKAG 657

Qy 659 YTEKORRDFLSEASTMGQFDHPNVHLRGVVTKTPVMIITEFMENGLSDFLRQNDQGF 718
Db 658 YSEKORRDFLSEASTMGQFDHPNIIIRLEGVVKRGPVMIITEFMENGLSDFLRQNDQGF 717

Qy 719 TVIQLVGLMGLGIAAGMKYLAADNMYVHRDLAARNLVNSNLVCKYVDSDFGLSRFLBEDDTSDP 778
Db 718 TVIQLVGLMGLGIAAGMKYLSMNVYVHRDLAARNLVNSNLVCKYVDSDFGLSRFLBEDDTSDP 777

Qy 779 TVTSLAGKQKIPIRWTAPPAIQAIRKFTSADSVSYGVIMVMEVSYGEPYDWTNQDVINA 838
Db 778 TVTSSLLGGKIPVRWTAQAIARFTSADSVSYGVIMVMEVSYGEPYDWTMSQDVINA 837

Qy 839 ISQDYRLPPMDPCSPALHOLMDCWQKRNRPKFGQIVNTLDKMRPNLSIKAMAPLSS 898
Db 838 IEQDYRLPPMDPCPAALHOLMDCWQKRNRPKFPRAEIVNTLRPMIRNPASLKTATIPA 897

Qy 899 GINLLPDLORTPYDTSFNVTDEWLEAIKVGQYKESFANAGTFSFVVSQMMEDILRLGV 958
Db 898 VPSQPLLDRSIPDISAFTSDVDDLSAIKMGQYRDNFLSSGFTSLQVLAQMTSEDLLRIGI 957

Qy 959 TLAGHOKKILNSIQWRAQMNIQ 980
Db 958 TLAGHOKKILNSIQSMRVQITQ 979

RESULT 5
150612
protein-tyrosine kinase (EC 2.7.1.112) Cek6 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
C:Accession: I50612; S33503
R:Sajjadi, F.G.; Pasquale, E.B.
Oncogene 9, 1807-1813, 1993
A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.
A:Reference number: I50611; MUID:93288394; PMID:8510926
A:Accession: I50612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-952 <SAJ>
A:Cross-references: EMBL:Z19110; NID:g312901; PIDN:CAA79526.1; PID:g312902
C:Genetics:
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin
F:585-853/Domain: protein kinase homology <KIN>
F:593-601/Region: protein kinase ATP-binding motif
F:876-942/Domain: SAM homology <SAM>

Query Match 71.8%; Score 3724; DB 2; Length 952;
Best Local Similarity 70.3%; Pred. No. 5.9e-163;
Matches 688; Conservative 121; Mismatches 118; Indels 52; Gaps 3;

Qy 21 ETLMDSTTATAELGWMVHPSPGSEVSGYDENMTIRYQV CNVFESSONNWLRTKFIIR 80
Db 1 ETLMDSTTATAELGWTANPPSGGEEVSGYDENMTIRYQV CNVFEPNQNLLTFINR 60

Qy 81 RGAHRHVENKFSVRDCSSIPSPGSCKETFNLYYYEADFDPSATKTFPNNMNPVVKVD 140
Db 61 RGAHRIVTEKFTVRDCSSLPNVPSCKETFNLYYYETDSVIATKKSASFTEAPYLKVD 120

Qy 141 IAADESFQVDLGGRVKINTEVRSFGVSRSGFLAFQDYGCMSLIAVRVYRKCPI 200
Db 121 IAADESFQVDLGGRLMK-----GXFFKCKPSV 148

Qy 201 IONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKAGF 260
Db 149 VONFAIFPFTWTGAESTSLVTARGTCIPNAEEVDVPIKLYCNGDGEWVPIGRCTKAGY 208

Qy 261 EAVENGTVCRGCPGSGTFFKANQGDGDEACTHCPINSRTTSEGATNCVCRNGYRADLPLDMP 320
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RESULT 7

S37627

protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C/Accession: S37627

R/Boehme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ruebs

Oncogene 8, 2857-2862, 1993

A/Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.

A/Reference number: S37627; MUID:9330963; PMID:8397371

A/Accession: S37627

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-998 <BOE>

A/Cross-references: UNIPROT:P54753; EMBL:X75208; MID:g406867; PIDN:CAA53021.1; PID:g406867

C/Suprafamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C/Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

F/631-899/Domain: protein kinase homology <KIN>

F/631-899/Region: protein kinase ATP-binding motif

F/922-998/Domain: SAM homology <SAM>

Query Match 70.6%; Score 3661.5; DB 2; Length 998;

Best Local Similarity 70.2%; Pred. No. 4.4e-160;

Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy	10	LLLLPLL-----AAVEETLMDSTTAAELGMVWHPSPGHEEYSGVDENMTTIRTYQVCN	63
Db	23	LLLLLLLLPAGCRALTEETLMDTKWVTSELAWTSHPESGWEESGYDEAMNPRTTYQVCN	82
Qy	64	VFSSQNNWLRTKFIERRGAHRTHVEMKFSVRDCSSIPSPGSKCTFNLYYEADPDSA	123
Db	83	VRESSQNNWLRTGFIWRDVQRYVELKFTVRDCNSIPNIPGSKCTFNLFYEADSDVA	142
Qy	124	TKTFPNMNPWKVDITIAADESFQVDLGGVRVWKINTEVRSFGPVSRSFGYLAPODYG	183
Db	143	SASSPPFWNPYKVDITIADESFSLRDAG----RVNVTKVSFGPLSKAGFYLAPODQA	198
Qy	184	CMSLIAVRYRKCPRIIQNGAIFQETLSGAETSLVAARGSCIANAEVDVPIKLYCNG	243
Db	199	CMSLISVRAPYKCASTTAGFALFPETLTGAETPSLVIAFPTCIPNAVESVPLKLYCNG	258
Qy	244	DGEWLVPGRCMCKAGPEAVENGVCRCGSGFTKANOQDEACTHCPINSRITSEGAATNC	303
Db	259	DGEWVVPVGACTCATGHEPAKESQCRPCPGSYKAKQGEGLCPCPNRSRTTSPASIC	318
Qy	304	VCRRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDIAYNIICK	363
Db	319	TCHNPFYRADSDADSACTVPBPGRGVISNVNETSLILEWSEPRDLGVRRDLLNVVICK	378
Qy	364	SC--GSGRGACTRCGDNVQAPQLGTEPRRIYISDLAHTQYTFEQAANGVTDQSPFS	421
Db	379	KCHGAGGASACSRDDNVFVPRQLGSEPRVHTSHLLAHTRYTFEQAANGVSGKSLP	438
Qy	422	PQASVNITTNQAAPSASVIMHQVSRVTDSITLWSOPDOPNGVILDYELQYKEKSELSEY	481
Db	439	PRVAVNITTNQAAPSEVPTIRLHSSGSSLTLSWAPPENGVILDIYEMKYEK--SEG	496
Qy	482	NATAIKSFPTNTVTVQGLKAGAIYVQVRAETVAGYGRYSKMYFQTMTE--AEYQTSIQEK	540
Db	497	IASVTVSQMSNVQLDGLRDPARYVQVRAETVAGYGRYSRPAEFETTSRSGGAQQLQEQ	556
Qy	541	LPLIIGSAGLVLPLIAVWIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF	600
Db	557	LPLTVGSATAGLVFVVAWVIAIVCLRKQHGSDSEYTEKLQY----IAPGMKVIYIDPF	612
Qy	601	TYEDPNEAVREFAKEIDISCVKIKBOVIGAGEFGVCSCHLKLPKGRIFVVAIKTLKSGYT	660
Db	613	TYEDPNEAVREFAKEIDVSCVKIEVLIGAGEFGVCGRLLKQPGRRVFAIKTLKGYIT	672
Qy	661	EKQRRDFLSASIMQDPHPNVHLEGVVTKSTPVMIIITTFMENGSLDSFLRQNDGGFTV	720

Db 673 ERQRDFLSEASIMQGFDPHPNIIRLEGVVTKSRPVMILTFMENCALDSFLRLNDGQFTV 732

Qy 721 IQLVGLRGIAAGKYLADMYNVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSDEPT 780

Db 733 IQLVGLRGIAAGKYLSEMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDPSDEPT 792

Qy 781 TSALGGKIPIRWTAPEAIORYKFTSASDVWSYGIYVMEVMSYGERPYWDMTNQDVINAIE 840

Db 793 TSSLGGKIPIRWTAPEAIAYRKFTSASDVWSYGIYVMEVMSYGERPYWDMNSQDVINAIE 852

Qy 841 QDYRLPPMDCPSALHQLMDCWQDRNHRPKFGQIVNTLTKMIRPNSLKAMAPLSSGI 900

Db 853 QDYRLPPMDCPTALHQLMDCWVRDNRNLRPKFSQIVNTLTKLIRNAASLUKVITASAQSGM 912

Qy 901 NLPLLDRTPDYTSFNTVDEMLEAKMGQYKESFANAGFTSFVWSOMMEDILRLGVTL 960

Db 913 SQPLLDRTPDYTTFTTVDGLWDLAKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972

Qy 961 AGHQKILNSIQVMRAQNMNQIOSVEV 986

Db 973 AGHQKILLSIQDMELQNMOTLPVOV 998

RESULT 8

I48653

mouse developmental kinase 5 (MDK5) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48653

R:Ciossek, T.; Lerch, M.M.; Ullrich, A.

Oncogene 11, 2085-2095, 1995

A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two novel

A:Reference number: I48652; MUID:96074837; PMID:7478528

A:Accession: I48653

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-993 <RES>

A:Cross-references: UNIPROT:P54754; EMBL:Z49086; NID:g1089899; PIDN:CAA88910.1; PID:g108

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C:Keywords: ATP; transmembrane protein

F:626-894/Domain: protein kinase homology <KIN>

F:634-642/Region: protein kinase ATP-binding motif

F:917-983/Domain: SAM homology <SAM>

Query Match 70.0%; Score 3630.5; DB 2; Length 993;

Best Local Similarity 69.8%; Pred. No. 1.le-158;

Matches 690; Conservative 113; Mismatches 165; Indels 21; Gaps 6;

Qy 9 ALLLLPLLA-----AVEETLMDSTTATAELGMVHPFSGWEEVSGYDENMNTIRTYQVCN 63

Db 15 APLLLPLLLPAGCWALEETLMDTKVTSSELAWTSHPESGWEEVSGYDEAMPIRTYQVCN 74

Qy 64 VFESQNNWLRTKFTRRRGAHRIHVEMKFSVRDCSSIPSVPGSKETFNLYVVEADPDSA 123

Db 75 VRESSQNNWLRTGFTWRREVQVYVVELKFTVRDCNSIPNIPGSKETFNLYVVEADSDVA 134

Qy 124 TKTRPNMNMVWKVDYTTAADSFSQVDLGGRWKINTEVRSFGPVSRSFGYLAFAQDYGG 183

Db 135 SASPEFWMENPVKVDYTTAPDSFSRLDAG----RVNWKVRSFGPLSKAGFYLAFAQDGA 190

Qy 184 CMSLIARVYFKPCRIIQNGAIFQTLTSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243

Db 191 CMSLISVRAGDKKCASTTAGAFALFPETLTGAETPSLVIAPGTCIANAEVSVPLKLYCNG 250

Qy 244 DGEWLVPICRCMKAGFAVENGTVCRCGSPGTFKANKQGDCACTHCPINSRTTSEGTATNC 303

Db 251 DGEWMVPVGCATCATGHEPAAKESQACRPPGSKAKQGGCPCLPCPNRSTTSPAAASIC 310

Qy 304 VCRNGYYRADLPLDWPCTTIPSAQVAVISSVNNETSLMLEWTPPRDSGGRDLVYNIICK 363

Db 311 TCHNNFYRADSDASACTTESPPGIVSNVNETSLLEWSEPRDLGGRDDLLYNVICK 370

Qy 364 SCGSGRGA-----CTRCGNQVAPRQLGLTEPIIVISDLLAHTQYTFEIQAVNGVTQDS 418

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Db 371 KCRSSGAGGATCSRCDNVEFVPRQLGLTERVHSHLLAHRYTFEVOANGVSGKS 430
Qy 419 PFSQFASVNTTNOAAPSAVSIHQVSRVTDSITLWSQDPQDPNGVILDYELQYKEKL 478
Db 431 PLPRYAANVTITNOAAPSEVPTLHSSSSGSLTSLWAPERNVNGVILDYEMKYFEK-- 488
Qy 479 SEYNATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGRYSGKQYFQWTE-AEYQTSI 537
Db 489 SKGIASVTQKNSVQLDGLQPDARYVQVRAARTVAGRYSGKQYFQWTE-AEYQTSI 548
Qy 538 QEKLPLIIGSAAGLVFLIAVVTIAVCNRRGFERADSEYTDKLOHYTSGHMTGKMIYI 597
Db 549 QEQLPLVIGSVAGVFMVMMVVIALVCLRKQRHGPDAEYTEKLQYQY----IAPGMKYI 604
Qy 598 DPFTYEDPNEAVREFAKEIDISCVKIEVIGAGFGEVCSGHLKPGKREIFVAKTLKS 657
Db 605 DPFTYEDPNEAVREFAKEIDISCVKIEVIGAGFGEVCSGHLKPGKREIFVAKTLKV 664
Qy 658 GYTEKQRDFLSEASIMQDPHPNVHLLEGVVTIKSTPVMITFPMENGLSDSFLRQDQG 717
Db 665 GYTEKQRDFLSEASIMQDPHPNIIRLEGVVTIKSRPVMILTEPMENCALDSFLRNDGQ 724
Qy 718 FTVLQVGLRGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSD 777
Db 725 FTVLQVGLRGIAAGMKYLSEMYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDPDS 784
Qy 778 PTTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVIN 837
Db 785 PTTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVIN 844
Qy 838 AIEQDYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDMKIRNPNLSKAMAPLS 897
Db 845 AVEQDYRLPPMDCPTALHQLMDCQKDRNHRPKFGQIVNTLDMKIRNPNLSKAMAPLS 904
Qy 898 SGINLPLDRTIPYTSFNTVDEWLEAKQYKESFANAGFTSFVDVVSQMMEDIIRLG 957
Db 905 SGMSQPLDRTIPYTSFNTVDEWLEAKQYKESFANAGFTSFVDVVSQMMEDIIRLG 964
Qy 958 VTLAGHOKKILNSIQVMAQNMQIQSVVEV 986
Db 965 VTLAGHOKKILNSIQVMAQNMQIQSVVEV 993

RESULT 9
I49071
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
A;Reference number: I49071; MUID:95200796; PMID:7893599
A;Accession: I49071
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-938 <RES>
A;Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F;571-839/Domain: protein kinase ATP-binding motif
F;579-587/Region: protein kinase ATP-binding motif
F;862-928/Domain: SAM homology <SAM>

Query Match 66.3%; Score 3441; DB 2; Length 938;
Best Local Similarity 68.9%; Pred. No. 4.9e-150;
Matches 653; Conservative 113; Mismatches 166; Indels 16; Gaps 6;

Qy 45 EVSGVDENMTIRYQVNCVPESSONWLRKTFIRRRGAHRIHYEMKFSVRDCSSIPSVP 104
Db 1 EVSGDEAMNPIRTYQVNCVPESSONWLRKTFIRRRGAHRIHYEMKFSVRDCSSIPSVP 60
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Qy 105 GSKCTENLNYEADFDSATKTFPNMNMENPWKVDVTITAADESPSQVDLGGVWKINTEVR 164
Db 61 GSKCTENLNYEADSDVASASSPFWMENPVYKVDVTITSPDESFSR--SMPGRV---NTRKV 116
Qy 165 SFGPVSBSGFLAFQDYGCGMSLIAVRFVYKCPRI11ONGAIFOETLSGAEASTSLVAARG 224
Db 117 SFGPLSKAGYFLGFQDQACMSLISVRAFVYKCASTTAGTALFPETITUGAETSLV1APR 176
Qy 225 SCIANAEVDVPIKLYCNGDGEWLPIGRCKAGFEAVENGTVCRCGSPGTFKANKQDE 284
Db 177 ACIANAEVSVPLKLYCNGDGEWVPGVACTGHEPAAKESQCRACPPGSKYKAKQEG 236
Qy 285 ACTHCPINSTTSEGATNCVRNGYTRADLDLPDMPCTTIPSPAQVIVSSVNETSLMLEW 344
Db 237 PCLPCPNSTRTTSPAASICTCHNFRADSDSADTCTRRSPPRGIVSNVNETSLLEW 296
Qy 345 TPRDSGGREDLVNIIKSCSGRGA-----CTRCGDNVQYAPRQLGLTEPRIYISDLL 399
Db 297 SEPRDLGGRDLLVNIICKRCRGSSGAGGATCSRCDNVEFVPRQLGLTERRVHSHLL 356
Qy 400 AHTQYTFEIOAVNGVTDQSPFSQFASVNTTNOAAPSAVSIHQVSRVTDSITLWSQP 459
Db 357 AHTRYTFEIOAVNGVSGKSPLPYRAAVNTTNOAAPSEVPTLHSHSTSGSLTSLWAPP 416
Qy 460 DQNGVILDYELQYKEKSEYNATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGRY 519
Db 417 ERPNGLVILYEMKYFEK--SKAIASVTQKNSVQLDGLQPDARYVQVRAARTVAGRY 474
Qy 520 SGRMYFQWTE-AEYQTSIOEKLPLIIGSAAGLVFLIAVVTIAVCNRRGFERADSEY 578
Db 475 THPAEFETTSERGSAQQLQEQPLVIGSNVAGVFMVMMVVIALVCLRKQRHGPDAEY 534
Qy 579 DKLQHYTSGHMTGKMIYIDPFTYEDPNEAVREFAKEIDISCVKIEVIGAGFGEVCSG 638
Db 535 EKLQYQY----IAPGMKYIIDPFTYEDPNEAVREFAKEIDISCVKIEVIGAGFGEVCSG 590
Qy 639 HLKLPGRKREIFVAKTLKSGYTEKQRDFLSEASIMQDPHPNVHLLEGVVTIKSTP 698
Db 591 RLKLPGRREVFVAKTLKVGYTEKQRDFLSEASIMQDPHPNIIRLEGVVTIKSRP 650
Qy 699 TEFMENGSLDSFLRQDQFTVLQVGLRGIAAGMKYLADNMVYVHRDLAARNILVNSNL 758
Db 651 TEFMENCALDSFLRNDGQFTVLQVGLRGIAAGMKYLSEMYVHRDLAARNILVNSNL 710
Qy 759 VCKVDFGLSRFLEDDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWME 818
Db 711 VCKVDFGLSRFLEDDPDSPTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWME 770
Qy 819 VMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVN 878
Db 771 VMSYGEQPYWMSNQDDINAVEQDYRLPPMDCPTALHQLMASCWVRDRNLRPKFSQIVN 830
Qy 879 TLDKMTIRNPNLSKAMAPLSGINLPLDRTIPYTSFNTVDEWLEAKQYKESFANAG 938
Db 831 TLDKLRNAASLKVTAAPSGMSQPLDRTIPYTSFNTVDEWLEAKQYKESFANAG 890
Qy 939 FTSFDDVVSQMMEDIIRLGVTTLAGHOKKILNSIQVMAQNMQIQSVVEV 986
Db 891 FASFDLVQAQMTAEDLLRIGVTLVGHQKILCSIQDMRLQNMQLPVQV 938

RESULT 10
I51549
receptor tyrosine kinase - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R;Winning, R.S.; Sargent, T.D.
Mech. Dev. 46, 219-229, 1994
A;Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1
A;Reference number: I51549; MUID:95001564; PMID:7918105
A;Accession: I51549
A;Status: preliminary; translated from GB/EMBL/DBJ
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[illegible][illegible]

Db 553 VSVTVGVILLAVIGVLLSGRCGYSKAQDPBEEKMHFNHGHKLPVGRVYIDPHTYED 612
Qy 605 PNEAVRFAKEIDISCVKIQVIGAGFVGVCSGHLKLPGRKIFVAIKTLKSGYTEKOR 664
Db 613 PNOAVHEFAKEIEASCITIBRVIGAGFVGVCSGRLKLPGRKELPVAIKTLKGYTEKOR 672
Qy 665 RDLSEASIMQGDHPHNVHLEGVVTSTPVMIIIFEMENGSLDSFLRQNDGQFTVIQLV 724
Db 673 RDLFGEASIMQGDHPHNVHLEGVVTSTPVMIIIFEMENGSLDTFLKXNDGQFTVIQLV 732
Qy 725 GMLRGIAAGKYLADMMYVHRDLAARNILVNSNLVKVDFGLSRFLDDTSDPTYSAL 784
Db 733 GMLRGISAGKYLSDMGYVHRDLAARNILVNSNLVKVDFGLSRFLDDTSDPTYSAL 790
Qy 785 GGIPIRWTAPALQYRKFTSASDVWSYGVIMVEMVSGRYPYDMTNQDVINAIEQDYR 844
Db 791 GGIPIRWTAPALQYRKFTSASDVWSYGVIMVEMVSGRYPYDMTNQDVINAIEQDYR 850
Qy 845 LPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSGGINLPL 904
Db 851 LPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSGGINLPL 910
Qy 905 LDRTPIDYTSFNTVDEWLEIAIKGOYKESFANAGFTSFVVSQMMEDIIRLGVTLAGHQ 964
Db 911 AEHSPLSGAGYRSVGEWLEIAIKGRYTEIFEMENGYSMDAVAQVTLDRRLGVTLVGHQ 970
Qy 965 KKIILNSIQVMRAQM 978
Db 971 KKIILNSIQVMRAQM 984

RESULT 12
178844
receptor protein-tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I78844
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janseen, A.M.; Basu, R.; Welcher,
Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty
A;Reference number: I58351; MUID:95206782; PMID:7898931
A;Accession: I78844
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-986 <RES>
A;Cross-references: UNIPROT:P54764; GB:I36645; NID:G551613; PIDN:AAA74246.1; PID:G551614

Query Match 58.7%; Score 3045; DB 2; Length 986;
Best Local Similarity 59.3%; Pred. No. 6.3e-132;
Matches 580; Conservative 146; Mismatches 112; Indels 40; Gaps 12;

Qy 18 AVETLMDSTATAELGCMVHP-PSGWEEVSGVDENNTTIRTVQVNCVVFSSQNNWLRTX 76
Db 28 ANEVTLDSRVSOGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVNCVNFPSQNNWLRTD 87
Qy 77 FIRRRAHRIHVMKFSVRDCSSIPSPVSGCKETFNLYYEADPDSATKTFPNWMPV 136
Db 88 WITREGAQRVYIEKFTLRDCNSLPVWGTCETFNLYYESSNDKERFI----RENQFV 143
Qy 137 KVDTIADESFQVDLGGRVNWKINTEVRSFGVSRSGFYLAPODYGCMSLIAVRVYRK 196
Db 144 KIDTIADESFTQVDIGDRIMKLNTEIRDVGLPSKKGFLAFQDVGACIALVSVRVYFK 203
Qy 197 CPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWELPIGRCMC 256
Db 204 CPLTVRNLAQFPDPTITGADTSSSLVEVRGSCVNNSEKQVDP-KMYCGADGELWLPVIGNCLC 262

Qy 257 KAGFEAVENGTVCRGCPSGTFRKANQGEAEATHCPINSRTTSEGATNCVCRNGYYRADLDP 316
Db 263 NACHE--ERSGEOACKIGYVKALSTDATCAKCPHPSYSVMEGATSTCTCRGFFRADNDA 320
Qy 317 LDMPTTIISAPQAVISSVNETSLMLEWTPPRDSGGREDLVNIIICKSCSG--RGATRC 375
Db 321 ASMPCTRPSPAPLNLISNVNETSVNLEWSPQNTGGRQDISYNVWCKKCGAGPFSKCRPC 380
Qy 376 GDMVOYAPROGLTEPRIYISDILLAHTQYTFEIQAVNGVTDQSPFSPQFASVNIITNQA 435
Db 381 GSGVHTYTPQNGLKTKTKVSTIDLLAHTNYTFELWAVNGVSKYNNPDPQSVVTVTNQA 440
Qy 436 PSASIMHQVSRVDSITLSWQDPDPNGVILDYELQYKEKSEYNATAIKSPTNTVT 495
Db 441 PSSIALVQAEKVTYRSVALAWLEPDRPNGVILEYEVKYKEKQNSRYRIVTAARNTDI 500
Qy 496 QGLKAGAIYVQVARTVAGYGRYSKMYFQTMTEAEYQTSIQEKLPL-LIIGS----- 547
Db 501 KGLNPLTYSYVHVRATAAGYGFDSPLFVNTT-----VPSRIIGCANSTVL 549
Qy 548 --SAAGLVFLLIAVWIAIVCNRR--GFERADSEYTDKLQHYTSGHMTPGMKIYIDPPTYE 603
Db 550 LVSVSQSVLVVLLIAAFVISRRRSKYSKAKQADEE-----KHLNQGVRTVVDPTYE 603
Qy 604 DPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKIFVAIKTLKSGYTEKQ 663
Db 604 DPNOAVREFAKEIDASCIKIEKVIGVGEFGEVCSGRLKVPGRKIFVAIKTLKAGYTDKQ 663
Qy 664 RRDFLSEASIMQGDHPHNVHLEGVVTSTPVMIIIFEMENGSLDSFLRQNDGQFTVIQL 723
Db 664 RRDFLSEASIMQGDHPHNVHLEGVVTSTPVMIIIFEMENGSLDAFLRKNDRGRFTVIQL 723
Qy 724 VGMLRGIAAGKYLADMMYVHRDLAARNILVNSNLVKVDFGLSRFLDDTSDPTYSA 783
Db 724 VGMLRGISAGKYLSDMGYVHRDLAARNILVNSNLVKVDFGLSRFLDDTSDPTYSA 782
Qy 784 LGGKIPIRWTAPALQYRKFTSASDVWSYGVIMVEMVSGRYPYDMTNQDVINAIEQDY 843
Db 783 -GGKIPIRWTAPALQYRKFTSASDVWSYGVIMVEMVSGRYPYDMTNQDVINAIEQDY 841
Qy 844 RLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSGGINL 903
Db 842 RLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKRTGTSSSRNTA 901
Qy 904 LLDRTIPDYTSFNTVDEWLEIAIKGOYKESFANAGFTSFVVSQMMEDIIRLGVTLAGH 963
Db 902 LLDPSGFSPFSAVSVSGDWLQAIKMDRYKDNFTAGYTTLEAVVHVNQEDLARIGITAIH 961
Qy 964 QKKILNSIQVMRAQMNOI 981
Db 962 QNKILSVQAMRTQMOM 979

RESULT 13
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: S78059; S30505; I58366
R;Charnay, P.
submitted to the EMBL Data Library, March 1992
A;Reference number: S78059
A;Accession: S78059
A;Molecule type: mRNA
A;Residues: 1-986 <CHA>
A;Cross-references: UNIPROT:Q03137; EMBL:X65138; NID:G54083; PIDN:CAA46268.1; PID:G54084
R;Gillard-Henstenreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson,
Oncogene 7, 2499-2506, 1992
A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t
A;Reference number: S30496; MUID:93096484; PMID:1281307
A;Accession: S30505
A;Molecule type: mRNA
A;Residues: 1-31,55-986 <GIL>

844 RLPPMDPCSPALHQLMLDCWKDRNRPKFGQIVNTLTKMIRNPNSLKAMAPLSSGINLP 903
842 RLPPMDPCPIALHQLMLDCWKERSDRPKFGQIVNMLDKLIRNPNSLKRGTSSSPNTA 901
904 LLDRTPIDYTSFNTVDWLEAIAKQYKESFANAGTSPDVVSOMMEDILRGVTLAGH 963
902 LLDPSSEFSAVSVSGDWLQAIKMDYKDNFTAAGYTTLLEAVVMSQDDILARIGITAIH 961
964 QKILNSIQVNRAMNOI 981
962 QNKILSSVQAMRTQOM 979

RESULT 14
158351
receptor protein-tyrosine kinase - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58351
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty A:Reference number: I58351; MUID:95206782; PMID:7898931
A:Accession: I58351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-998 <RES>
A:Cross-references: UNIPROT:Q15375; GB:L36642; NID:9551607; PIDN:AAA74243.1; PID:9551608
C:Genetics:
A:Gene: HEK11
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C:Keywords: ATP; transmembrane protein
F:631-897/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:920-986/Domain: SAM homology <SAM>

Query Match 58.4%; Score 3028; DB 2; Length 998;
Best Local Similarity 59.1%; Pred. No. 3.8e-131;
Matches 574; Conservative 153; Mismatches 224; Indels 20; Gaps 9;

17 AAVEETLMDSTTATAEALGMVHPSPGWEVSGYDENMTIRTYQVCNFPSSQNNLRTK 76
29 AAKEVLLDSKAQTELEWISSPPNGWBEISGLDENYTPIRTYQVCNFPNNLRTN 88
77 FIRRGAHRIHVMKFSVDCSSIPVSGCKETNLVYEAADFSATKTFENMMENPW 136
89 WISGNAQRIFFVELKFTLRDCNSLPGLCTKETNLVYETDYD---TGNIRENLV 144
137 KVDITAADESFSQVDLGRVMKINTEVRSFPGVSRSGFYLAQDYGGCMLTAVRVYRK 196
145 KIDITAADESFTQDGLGERKMLNTEVREIGPLSKKGFYLAQDVGCIALVSVKYKK 204
197 CPRIIONGAIQFTLSGAESTSLVAARGSCIANA-BEVDVPIKLCNGDGEWLVPICGM 255
205 CWSIIENLAIFPDVTGTSFSSLVVRGTCVSSABEENAPRMHCSEAGELWLPKICI 264
256 CKAGFEAVENGTCRCGCPCTFKANQGDCACTHCPINSRTTSEGATNCVCRNGYRADLP 315
265 CKAGYO--QKGDTCPCGRCGFYKSSQDLCQSCPTHSFSDKXSSRCECDGYRAPSD 322
316 PLDMPTCTTIPSAQVAVISSVNETSLMELWTPPRDSCGREDLVNIIKSCGSRGACTRC 375
323 PPVACTRPSPAPQNLIFNINQTTVSLWSPPPADNGRNDVYRILCKRCSWEQGCVCPC 382
376 GDNVQYAPRGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFSAVNITNQAA 435
383 GSNTRYPMQPTGLEEDNTVVDLLAHANYTFEVAENVGSDLSRSQRLFAAVSITTGAA 442
436 PSVSIHQVSRVTSDITLSWSPQDPQNGVILYQYKELSEYNATAIKSFTVTIV 495
443 PSQVSGWKERVLQSRSELSWQEPHNGVITEYIKYEKQDQRTYSTVTKTSASI 502
496 QGLKAGAIYVQVAPRIVAGYGRSGKMYFTQTEA-----EYQTSIQEKLPLIGS--S 548

A:Cross-references: EMBL:X65138
C:Gene: Sek
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F:548-569/Domain: transmembrane #status predicted <TM>
F:627-635/Region: protein kinase homology <KIN>
F:908-974/Domain: SAM homology <SAM>
F:235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.6%; Score 3040; DB 2; Length 986;
Best Local Similarity 59.3%; Pred. No. 1.1e-131;
Matches 580; Conservative 148; Mismatches 210; Indels 40; Gaps 13;

18 AVEETLMDSTTATAEALGMVHP-PSGWEVSGYDENMTIRTYQVCNFPSSQNNLRTK 76
28 ANEVTLLDSRVOGELGWIAPLEGGWBEVSIMDEKNTPIRTYQVCNWEASQNNLRTD 87
77 FIRRGAHRIHVMKFSVDCSSIPVSGCKETNLVYEAADFSATKTFENMMENPW 136
88 WITREGAQRVIEIKFTLRDCNSLPFGWICKETFNLYYESDNDKERFI---RESQFG 143
137 KVDITAADESFSQVDLGRVMKINTEVRSFPGVSRSGFYLAQDYGGCMLTAVRVYRK 196
144 KTDITAADESFTQDGLGRIMKLNTEIRDVGLSKKGFYLAQDVGCIALVSVRVYRK 203
197 CPRIIONGAIQFTLSGAESTSLVAARGSCIANAEBVDVPIKLCNGDGEWLVPICRCM 256
204 CELTVRNLAQPDITIGADTSLVEVRGSCVNNSEKQVDP-KMYCGADGEWLVPICNLC 262
257 KAGFEAVENGTCRCGCPGTFKANOQDEACTHCPINSRTTSEGATNCVCRNGYRADLP 316
263 NAGHEE-QNGE-CQACKIGYKALSTASCACPPHSYVWEGATCTCGRGFRAND 320
317 LMPCTTIPSAQVAVISSVNETSLMELWTPPRDSCGREDLVNIIKSCGSG-RGACTRC 375
321 ASMPCTRPSPAPNLINSVNETSLVNLWSSPQNTGGRQIDISYNNVCKKAGDPSKCRPC 380
376 GDNVQYAPRGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFSAVNITNQAA 435
381 GSGVHTPOONGLKTRVSI TDLAHTNYTPEIWA VNGVSKYNSPDQSVTVTTNQAA 440
436 PSVSIHQVSRVTSDITLSWSPQDPQNGVILYQYKELSEYNATAIKSPNTVTV 495
441 PSSIALVQAKEVTRYSVLAWLPRDPNGVILEYEVKYKQDQNERSTRIVRTAARNTDI 500
496 QGLKAGAIYVQVAPRIVAGYGRSGKMYFTQTEAETQTSIQEKLIP-LIIGS----- 547
501 KGLNPLTSTVYVHVRATAAGYDFSEPLEVTNT-----VPSRIIGDGANSTVL 549
548 --SAAGLVFLIAVVAIVCNRR--GFERADSEYTDKLOHYTSGMTQMKIYIDPFYVE 603
550 LVSVSGSVLVILIAAFVISRRRSKYSAKQEADEE-----KHLNQGVRYVDPFYVE 603
604 DPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKLKSQYTBKQ 663
604 DPNAVREFAKEIDASCICKIERVIGGEFGEVCSGHLKVPKREICVAIKLKAGYTDKQ 663
664 RRDFLSASIMGQDPHNIIHLGSGVTKCPVMIITEFMENGLSDFLRQNDGQFTVQL 723
664 RRDFLSASIMGQDPHNIIHLGSGVTKCPVMIITEFMENGLSDFLRQNDGQFTVQL 723
724 VGLMRGTAAGKYLADMYVHRDLAARNILVNSNLVCKVSDFLSLEDSDTPTTISA 783
724 VGLMRGTCGSKYLSDMYSYVHRDLAARNILVNSNLVCKVSDFLSLEDSD-PEAYTTR 782
784 LGGKIPRWTAPAEIAQVKEKTSASDVMSYGI VNWVMSYGERPYDWTQDVINAJEQDY 843
783 -GGKIPRWTAPAEIAQVKEKTSASDVMSYGI VNWVMSYGERPYDWTQDVIKALEEGY 841

Db 503 NNLKPGTVYVQIRAFIAFTAGYNTSPRLDVALESEATGKMPFAVASEQNPFVIAVVA 562
Qy 549 AAGLVFLIAVVAIAVCNRR--GPERADSEYTDKLOHTYTGHTMPGKIYIDPFYEDPNE 607
Db 563 VAGTILVFWVFGIIGRRHCGYSKADQGBELYFH---FKPGTKTYIDPTEYEDPNR 619
Qy 608 AVREFAKEIDISCVKIBQVIGAGFGEVCSGHLKLPKGRKREIFVAIKTLKSGYTEKQRDF 667
Db 620 AVHQFAKELDASCICKIERVIGAGFGEVCSGRLKLPKGRDVAVAIKTLKVGYTEKQRDF 679
Qy 668 LSEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGM 727
Db 680 LCEASINGQDHPNVHLEGVVTGKPMIVIEFMENGALDAPFLRKHGQFTVQLVGM 739
Qy 728 RGIAGMKYLAADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 787
Db 740 RGIAGMRYLAADMGVYHVRDLAARNILNSNLVCKVSDFGLSRVIEDD--PEAVYTTT--GGK 797
Qy 788 IPIRWTAPAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEODYRLPP 847
Db 798 IPIRWTAPAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMNSQDVKAIEBGRPLA 857
Qy 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMIARNPNSLKAMAPLSSGINPLD 907
Db 858 PMDCPAGLHQLMDCWQKDRABERPKFQIVGILDKMIARNPNSLKTPLGTCSRPI 917
Qy 908 TIPDYTEFNTVDEWLEAIKMGQYKESFANAGFTSDFVVSOMMEDILRLGVTLGHO 967
Db 918 NTPDFTTFCVSGEWLQAIKMYRYKDNFTAAAGNSLESVARMTIEDVMSLGLT 977
Qy 968 LNSIQVMRAQM 978
Db 978 MSSIQTMRAQM 988

RESULT 15
JC5672
receptor tyrosine kinase (EC 2.7.-.-) EbK precursor - mouse
N;Alternate names: developmental kinase 1
C;Species: Mus musculus (house mouse)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5672; I48611; S51740
R;Talukder, A.H.; Muramatsu, T.; Kanada, N.
Cell Struct. Funct. 22, 477-485, 1997
A;Title: A novel truncated variant form of EbK/MDKI receptor tyrosine kinase is expressed
A;Reference number: JC5672; MUID:98035156; PMID:9368721
A;Accession: JC5672
A;Molecule type: mRNA
A;Residues: 1-998 <TAL>
A;Cross-references: UNIPROT:Q61772
A;Experimental source: embryo
R;Glosser, T.; Millauer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A;Title: Identification of alternatively spliced mRNA encoding variants of MDKI, a novel
A;Reference number: I48611
A;Accession: I48611
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-998 <RGS>
A;Cross-references: EMBL:X79082; NID:9607133; PID:CAA55687.1; PID:9607134
C;Comment: This enzyme plays a role during development involving differentiation and pro
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; brain; phosphotransferase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-998/Product: receptor tyrosine kinase EbK #status predicted <MAT>
F;31-553/Domain: extracellular #status predicted <EXT>
F;331-438/Domain: fibronectin type III repeat <FN1>
F;441-534/Domain: fibronectin type III repeat <FN2>
F;554-579/Domain: transmembrane #status predicted <TM>
F;631-897/Domain: protein kinase homology <KIN>
F;639-647/Region: protein kinase ATP-binding motif
F;920-986/Domain: SAM homology <SAM>

Query Match 58.1%; Score 3013; DB 2; Length 998;
Best Local Similarity 58.6%; Pred. No. 1.8e-130;
Matches 572; Conservative 157; Mismatches 217; Indels 30; Gaps 11;
Qy 17 AAVEETLMDSTTAAELGVMWHPSPSGWEEVSGVDENMNTTIRTYOVVFNSSQNNWLRTK 76
Db 29 AAKEVLLDLSKAQOTELEWISPPSGWEEISGLDENYTPIRTYOVVFNSSQNNWLRTN 88
Qy 77 FIRRGAHRTHVMKPSVRDCSSIPSPVSGKCTFNLYYEADPDSATKTPPNMNPW 136
Db 89 WISKGNARLIFVELKFTLRDCNSLPGVLGCTKCTFNLYYETDYD----TGRNRENLV 144
Qy 137 KVDITIADESFSQVDLGGVRVMKINTEVRSFGPVSRSFGYLAFOYGGCMSLIAVRVYRK 196
Db 145 KIDTIAADESFTQDLGERKMKLNTREIGPLSKGFLAFQDVGVACIALVSVKVYVK 204
Qy 197 CPRIIONGALFOETLSGAESTSLVAARGCIANA--BEVDVPIKLYCNGDSEWLVPIGRM 255
Db 205 CWTIVENLAVFPDVTGTGSEFSLVEVRGTCVSSAAEEAENSPRMHCASBGEWLVPIGKI 264
Qy 256 CKAGFEAVENGTVCRGCPSGTFRANQGDCACTHCPINSRTTSEGATNCVCRNGYYRADLD 315
Db 265 CKAGIQ--QKGDCEPCRRFYKSSSQDLQSCRPTHSPDRREGSSCECEDGYRAPSD 322
Qy 316 PLDMPCPTTIPSAQVAVISSYNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTRC 375
Db 323 PPVYACTRPPSAQNLFINQITVSLWSPPADNGGRNDVYRILCKRCSWEQGEVCP 382
Qy 376 GDNVQAPROGLTEPRIYISDLAHTQYTFEQAQNGVTDQSPFQPFASVNTTQAA 435
Db 383 GSNIGYMPQQTGLEDNVYVMDLAAHANYTFEVAENVGSDLSRSQRLFAAVSITGQAA 442
Qy 436 PSASVIMHOVSRTVDSITLSWSOPDQNGVLDYELQYKEKSELSEYNATAIKSTNTVT 495
Db 443 PSQVSGVMKERVLRQSLSNQEPHENGVTETETIKYEDQREYRSTYIKTSTASI 502
Qy 496 QGLKAGAIYVQVRAVTVAGYGRYSGMYFQTMTEA-----EYQTSIQEKLPLIGS--S 548
Db 503 NNLKPGTVYVQIRAFIAFTAGYNTSPRLDVALESEATGKMPFAVASEQNPFVIAVVA 562
Qy 549 AAGLVFLIAVVAIAVCNRR--GPERADSEYTDKLOHTYTGHTMPGKIYIDPFYEDPNE 607
Db 563 VAGTILVFWVFGIIGRRHCGYSKADQGBELYFH---FKPGTKTYIDPTEYEDPNR 619
Qy 608 AVREFAKEIDISCVKIBQVIGAGFGEVCSGHLKLPKGRKREIFVAIKTLKSGYTEKQRDF 667
Db 620 AVHQFAKELDASCICKIERVIGAGFGEVCSGRLKLPKGRDVAVAIKTLKVGYTEKQRDF 679
Qy 668 LSEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGM 727
Db 680 LCEASINGQDHPNVHLEGVVTGKPMIVIEFMENGALDAPFLRKHGQFTVQLVGM 739
Qy 728 RGIAGMKYLAADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 787
Db 740 RGIAGMRYLAADMGVYHVRDLAARNILNSNLVCKVSDFGLSRVIEDD--PEAVYTTT--GGK 797
Qy 788 IPIRWTAPAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEODYRLPP 847
Db 798 IPIRWTAPAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMNSQDVKAIEBGRPLA 857
Qy 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMIARNPNSLKAMAPLSSGINL 902
Db 858 PMDCPAGLHQLMDCWQKDRABERPKFQIVGILDKMIARNPNSLKTPLGTCSRPLS----- 912
Qy 903 PLIDRTIPDYSFNTVDEWLEAIKMGQYKESFANAGFTSDFVVSOMMEDILRLGVTLG 962
Db 913 PLDQSTPDTAFCSGWLQAIKMYRYKDNFTAAAGNSLESVARMTIEDVMSLGLTAVG 972
Qy 963 HOKKILNSIQVMRAQM 978
Db 973 HOKKIMSSIQTMRAQM 988

RESULT 16
I50615
receptor-type protein-tyrosine kinase Cek7, long splice form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50615; I50616; I50614
R;Siever, D.A.; Verderame, M.F.
Gene 146, 219-226, 1994
A;Title: Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence
A;Reference number: I50614; MUID:95047429; PMID:7958948
A;Accession: I50615
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1013 <SIE>
A;Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PID:AAB60612.1; PID:95556
A;Accession: I50616
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-572, 'R', 596-1013 <S12>
A;Cross-references: EMBL:U03910; NID:9555617; PID:AAB60613.1; PID:9555619
A;Accession: I50614
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-279, 444-572, 'R', 596-1013 <S13>
A;Cross-references: EMBL:U03910; NID:9555617; PID:AAB60614.1; PID:9555620
C;Genetics:
A;Gene: Cek7
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: alternative splicing; ATP; transmembrane protein
F;649-915/Domain: protein kinase homology <KIN>
F;657-665/Region: protein kinase ATP-binding motif
F;938-1004/Domain: SAM homology <SAM>

Query Match 58.0%; Score 3009; DB 2; Length 1013;
Best Local Similarity 57.0%; Pred. No. 2.8e-130;
Matches 568; Conservative 165; Mismatches 229; Indels 34; Gaps 10;

QY 6 LGALLLLPLAAVEETLMDSTTATAEALGVMVHPSPGWEVSGYDENNTIRTYQVCNVF 65
DB 22 LCAALRLSLAGSGEWNLDRTVGLWIAFPKNGWEEIGEDVENVAPHTYQVCNVK 81
QY 66 ESSQNNWLRTKPIRRGAHRIHVMKFSVRDCSSIPSPGSKETFNLYYEADFDSATK 125
DB 82 EQQNNWLLTSWISNEGRPASSFELKFTLRDCNSLPGLGTCETFNMYFESDDEGR- 140
QY 126 TFPNMENPWKVDITIADESPQVDLGRVWKNITEVSPGVSRSQFYLAPODYCGCM 185
DB 141 ---NIRENOYIKIDITIADESFTLGLDRVWKNLTVRVDGVLTKGKGYLAFOVGACI 197
QY 186 SLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245
DB 198 ALVSVRVYKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 256
QY 246 EWLVPTRGCMKAGFEAVENGTVRCGSPGTFKANGQDEACTHCIPINRTTSEGATNCVC 305
DB 257 EWLVPTRGCMKAGFEAVENGTVRCGSPGTFKANGQDEACTHCIPINRTTSEGATNCVC 314
QY 306 RNYGYRADLDLDMPTTIPSAQAVISSVNETSLMLEWTPDRSGREDLVNIIICKSC 365
DB 315 BEHYFRRESDDPTMACTRPSPAPRAISNVNETSLVLEWIPADTGGKRDVSYIACKKC 374
QY 366 GSGRGACTCGNVQVAPQLGLTEPRIYISLLAHTQYTFEIOAVNGVTQSPSPQFA 425
DB 375 NHHSGLCACGSHRVLPQOTGLKNTSVNMVLLAHTNYTFEIAVNGVSDQNPQARQV 434
QY 426 SVNITNQAAAPSVAISMHOVSRVDSITLSWQPOPNQVILDLQYKELSEYNATA 485
DB 435 SVNITNQAAAPSVAISMHOVSRVDSITLSWQPOPNQVILDLQYKELSEYNATA 493
QY 486 IKSPTNTVTVQGLKAGAIYVFOVARTVAGYSGMYFQNTWAEYQTSIQEKLPLII 545
DB 494 IKSPTNTVTVQGLKAGAIYVFOVARTVAGYSGMYFQNTWAEYQTSIQEKLPLII 552

QY 546 GSSAAGLVFLIAVVVIAI---VCN-----RRGFERADSEYTDKLOH 583
DB 553 VSVTVGVILLAVVIGFLSGSCDHCWGASSLRVAVPSLIWRCGYSKAQDPDEEKOH 612
QY 584 YTSGHM-TPGMKIYIDPPTYEDPNVAREFAKEIDISCVKIEOVIGAGEFVCSGHKL 642
DB 613 FHNGHIKLPVGRVYIDPPTYEDPNVAREFAKEIDISCVKIEOVIGAGEFVCSGHKL 672
QY 643 PKRELFVAIKTLKSGYTEKORRDLFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFM 702
DB 673 QKREFFVAIKTLKSGYTEKORRDLFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFM 732
QY 703 ENGSLDSFLRQNDGQFTVIQLVGLMLRGIAAGMKYLAADNMYVHRDLAARNILVNSLVCKV 762
DB 733 ENGSLDTFLKNDGQFTVIQLVGLMLRGIAAGMKYLAADNMYVHRDLAARNILVNSLVCKV 792
QY 763 SDFGLSRFLEDDTSDPTTYSALGGKIPRTWAPAIAQYRKFTSASDVMSYGIWMVEVMSY 822
DB 793 SDFGLSRVLEDD-PEAAVTTR-GGKIPRTWAPAIAQYRKFTSASDVMSYGIWMVEVMSY 850
QY 823 GERPYDMTNQDVINAIEDYRLPPMDPCPSALHOLMLDCWQKDRNHRPKFQOIVNTLDK 882
DB 851 GERPYDMTNQDVINAIEDYRLPPMDPCPSALHOLMLDCWQKDRNHRPKFQOIVNTLDK 910
QY 883 MIRNPNSLKAMAPLSSGINLPLDRTIPDYSFNTVDWLEAIKMGQYKESFANAGFTSF 942
DB 911 LIRNPSSLATLVNASSRVSNLLVHSPVSGSAYRSVGEWLEAIKMGQYKESFANAGFTSF 970
QY 943 DVVSQMMEDILRLGVTLAGHOKKILNLSIQVNRQAM 978
DB 971 DSAQVTELEDRRLRGLTVLGHQKIMNSLQEMKQVL 1006

RESULT 17
S51604
receptor-like tyrosine kinase Etk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C;Accession: S51604
R;Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A;Reference number: S49015; MUID:94067777; PMID:7504232
A;Accession: S51604
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-981 <NAI>
A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif

Query Match 56.6%; Score 2939; DB 2; Length 981;
Best Local Similarity 58.3%; Pred. No. 4.3e-127;
Matches 552; Conservative 161; Mismatches 220; Indels 14; Gaps 10;

QY 6 LGALLLLPLAAVEETLMDSTTATAEALGVMVHPSPGWEVSGYDENNTIRTYQVCNVF 65
DB 48 LCAALRLSLAGSGEWNLDRTVGLWIAFPKNGWEEIGEDVENVAPHTYQVCNVK 107
QY 66 ESSQNNWLRTKPIRRGAHRIHVMKFSVRDCSSIPSPGSKETFNLYYEADFDSATK 125
DB 108 EQQNNWLLTSWISNEGRPASSFELKFTLRDCNSLPGLGTCETFNMYFESDDEGR- 166
QY 126 TFPNMENPWKVDITIADESPQVDLGRVWKNITEVSPGVSRSQFYLAPODYCGCM 185
DB 167 ---NIKQYIKIDITIADESFTLGLDRVWKNLTVRVDGVLTKGKGYLAFOVGACI 223
QY 186 SLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245

Db 224 ALVSRVYVYKCRSVVRHLAVPDTITGADSSQLLEVGSCV-NHSTVDDPPKMHCSAEG 282
Qy 246 EWLVPICRMCCKAGFAVENGTVCRCGPGSTGFKANQDEACTHCPINSRTTSETGATNCVC 305
Db 283 EWLVPICRMCCKAGYEE-KNGT-CQVCRPGFFKASPHSQICSKCPHSHYTHEEASTSCVC 340
Qy 306 RNGVYRADLDPLDMPCTTIPSAQAVTSSVNETSLMLEWTPPRDSGGREDLVNIIICKSC 365
Db 341 EKDYFRRESPPPTWACTRPPSPAPRNAISNVNETSVFLEWIPPADTGGGKDVSYILCKKC 400
Qy 366 GSGRGACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQEA 425
Db 401 NSHAGVCEBEGHVRVLPQQIGLKXNVSVMADPLAHTNYTFEIEAVNGVSDLSGTQYV 460
Qy 426 SVNITTTQAAPSASVIMHQSRTVDSITLSNSQDPQNGVILDYELQYKEISEYNATA 485
Db 461 SVNITTTQAAPSPVTVNKKGKIAKNSISLSQWEPDRNGIILEYIKFEK-QETSVTI 519
Qy 486 IKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIQBKPLII 545
Db 520 IKSKETTITAEGLKAPSVYVQIBARTAAAGYGFESRREFET-TPVFGASNDQSQIBIIG 578
Qy 546 GSSAAGLVFLIAVVIACVNRGRFERADSVTDKLOHTYSGH-TPGMKIYIDPFTYED 604
Db 579 VSVTVGVILL--AVMIGFLRCRGYSKAKQDPESEKWHFHGHILKPGVRTYIDPFTYED 636
Qy 605 PNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKOR 664
Db 637 PTQAVHEFGKEIBASCITISERVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKOR 696
Qy 665 RDLFSEASIMGQDPHPNVHLEGVVTKSTPMIITEPMENGSLDSFLRQNDGQRTYOLV 724
Db 697 RDLFSEASIMGQDPHPNIHLEGVVTKSKPMIITEPMENGSLDTFLKXNDGQRTYOLV 756
Qy 725 GMLRGIAGKYLADNVVHRLAARNILVNSNLVCKVSDGFLSRFLEDDTSDPTYSAL 784
Db 757 GMLRGIAGKYLSDMGVHRLAARNILVNSNLVCKVSDGFLSRVLEDD-PEAAVTR- 814
Qy 785 GGIPIRTWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEQDYR 844
Db 815 GGIPIRTWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEQDYR 874
Qy 845 LPPMDCPSALHQLMCDWQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGINLPL 904
Db 875 LPPMDCPSAALYQLMCDWQKDRNHRPKFDDVNNLKLIRNPNLSLKAMAPLSSGINLPL 934
Qy 905 LDRITPDTSTNTVDEMLEAKMGQYKESFANAGTSTFVVSOMME 951
Db 935 AEHSGSLGSAYRSVGEWLEATKMGRTYEIFMENGYSSMDAVAQVTL 981

RESULT 18
B45583
receptor tyrosine kinase Csk4 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B45583
R/Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A/Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
A/Reference number: A45583; MUID:92031278; PMID:1657122
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-983 <SAJ>
A/Cross-references: UNIPROT:P29318; GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:g211447
A/Note: sequence extracted from NCBI backbone (NCBI:62405, NCBI:62411)
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C/Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-895/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif

Query Match 56.5%; Score 2931; DB 2; Length 983;

RESULT 19

Best Local Similarity 56.2%; Pred. No. le-126;
Matches 552; Conservative 178; Mismatches 233; Indels 20; Gaps 9;

Qy 1 MALRRLLCAALLLLPLAA-----VEETLMDSTTATAELGMVWHPSPGWEVSGVDEN 52
Db 1 MDRRLRLLLLLCAALGAGRLSARPGNEVLLDSKTQGLGWLISYFSGHWEISGVDEH 60
Qy 53 MNTIRTYQVCNVFESSQNNWLRTKFIIRRGARHIVEMKFSVRDCSSIPSVPSCKETFN 112
Db 61 YTPIRTYQESNVMDHSQNNWLRTNWI PRNSAQKIYVELKFTLRDCNSIPLVLGCTCKTFN 120
Qy 113 LYIYEAQDFDSTKTFPMNMENPVKVDITIAADSFSDVLDGGRVMKINTVRSFGPVRS 172
Db 121 LYIMESDDDLHLAK----FREQHTFKIDTIAADESFQMDLGLDKLKLNTREVREPGVSKK 176
Qy 173 GFYLAFODYGGCSLIIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAE 232
Db 177 GFYLAFODVACVALSVRVYFKCPFTVKLAMPDTPV-MDSQSLVVEVGVSCVNSKE 235
Qy 233 VDVPILKLYCNGDGEWLVPICRMCCKAGFAVENGTVCRCGPGSTGFKANQDEACTHCPIN 292
Db 236 EEPK-KMYCSTEGEWLVPIGKCLCNAGYE--ERGFACQACRPGFYKASAGNVKCAKCPH 292
Qy 293 SRTTSEGATNCVCRNGYYRADLDPLDMPCTTIPSAQAVTSSVNETSLMLEWTPPRSGG 352
Db 293 SSTYEDASLNCRCCKNYFRSEKDPSPSMACRPPSPAPRNVISNINETSIVLDWSPLDTGG 352
Qy 353 REDLVNIIICKSGRGAGACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVN 412
Db 353 RKDVTNIIICKGGSSKICEPCSDNVRFLPRTGLTNTVTVVVDLAHTNYTFEIDAVN 412
Qy 413 GVTDSQSPFQFASVNTITNQAAPSASVIMHQSRTVDSITLSNSQDPQNGVILDYELQ 472
Db 413 GVSDDLSTLSRQFAAVSITTTQAAPSPTIVIRKORTSRNSVLSWQEPHEHNGIILDEYVK 472
Qy 473 YYEKEISEYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQTMTEAE 532
Db 473 YYEKEQOETSYTLRAKSTNTVTSGLKPDPTVYVQIPARTAAARYGTSRKFEPFETSPDS- 531
Qy 533 YQTSIQBKLPLIIGSSAAGLVFLIAVVIACVNRGRFERADSVTDKLOHTYSGH-TP 591
Db 532 FSTSSNSQVVMIAISAIAVAIILTVVYVYVIGRCFGYKSKGTDKRLHFGHGLKLP 591
Qy 592 GMIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVA 651
Db 592 GLRTYVDPTHYEDPNQAVHEFAKELDASNISIDKVVGAGFGEVCSGRLKLPKKEISVA 651
Qy 652 IKTLKSGYTEKORRDLFSEASIMGQDPHPNVHLEGVVTKSTPMIITEPMENGSLDSFL 711
Db 652 IKTLKAGYTEKORRDLFGEASIMGQDPHPNIHLEGVVTKSKPMIITEPMENGSLDSFL 711
Qy 712 RONDGQFTVIQLVGLRGLIAGMKYLADNVVHRLAARNILVNSNLVCKVSDGFLSRFL 771
Db 712 RKHDAQFTVIQLVGLRGLIAGMKYLSMGVYHRLAARNILVNSNLVCKVSDGFLSRVL 771
Qy 772 EDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMT 831
Db 772 EDD-PEAAVTR-GGIPIRTWTSPEAIYRKFTSASDWSYGIVLWEVMSYGERPYWEMS 829
Qy 832 NQDVINAIEQDYRLPPMDCPSALHQLMCDWQKDRNHRPKFGQIVNTLDMKIRNPNLSLK 891
Db 830 FQDVIRKAVDEGYRLPPMDCPSAALYQLMCDWQKDRNHRPKFQIVNIDKLIRNPNLSLK 889
Qy 892 AMAPLSSGINLPLDRTIPDTSTNTVDEMLEAKMGQYKESFANAGTSTFVVSOMME 951
Db 890 IITNAARPNLLDQNSINDISAFRTAGDMLNGFRTQCQKGIFTGVYSSCDTITAKISTD 949
Qy 952 DILRLGVTTLAGHQKILNSIQVM 974
Db 950 DMKKVGTVVVGPKKIVSSIKTL 972

616 LDATNISIDKVVAGBGEVCSGRLLPLSKKEISVAIKTLKVGYTEKQRDFLGEASIMG 675
676 QFDHPNVIHLEGVTKSTPMTITFPMENGLSDFLRQNDQFTVQLVGLMRLGIAAGMK 735
676 QFDHPNIIRLEGVTKSPVMTITFPMENGLSDFLRKHDQFTVQLVGLMRLGIAAGMK 735
736 YLADWVYVHRDLAARNILVNSLVCKVDFGLSRFLFDDTSDPTTYSALGKGIPIRWTP 795
736 YLSDMGVYVHRDLAARNILVNSLVCKVDFGLSRFLFDDTSDPTTYSALGKGIPIRWTP 793
796 EAIQYRKFTSASDVMSYGIWVMSYGERPYWDMTQDVINALEQDYRLPPMDCPAL 855
794 EAIAYRKFTSASDVMSYGIWVMSYGERPYWDMTQDVINALEQDYRLPPMDCPAL 853
856 HOLMLDCWQKDRNRPFGQLVNTLDKMRPNLSLKAMAPLSSGINILPLDRTIPDTYSF 915
854 YQLMLDCWQKDRNRPFGQLVNTLDKMRPNLSLKAMAPLSSGINILPLDRTIPDTYSF 913
916 NTVDWELAIKMGQYKESFANAGFTSPVWSQMMEDILRLGVTLAGHOKKILNSIQVMR 975
914 RTGDLNGLVARTACKEIFTGTVEYSCDTIAKISTDDMKVGVTVWGPQKKIISIKALE 973
976 AQ 977
974 TQ 975

RESULT 20
S49015
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S49015; S51602
R:Naissompierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777; PMID:7504232
A:Accession: S49015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MAI>
A:Cross-references: UNIPROT:P54757; EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:675-941/Domain: protein kinase homology <KIN>
F:683-691/Region: protein kinase ATP-binding motif

Query Match 56.3%; Score 2923; DB 2; Length 1005;
Best Local Similarity 57.2%; Pred. No. 2.4e-126;
Matches 555; Conservative 161; Mismatches 218; Indels 36; Gaps 12;

QY 6 LGAALLLLPLAAVEETLMDSTTATLGLWVHPSPGSEVSGVDENMTIRYQVCNVF 65
DB 48 LCAALRTLLASPSNEVNLDSRTVLGDLGWIAPFKNGWEEIGEVNDENYAPIHYQVCKM 107
QY 66 BSSONNNMLRTKIFRRGAHRIHVEMKFSVRDCSSIPSVPSCKETFNLYYYEADFDGATK 125
DB 108 EQONNNLLTSWISNEGASRLFIETKFTLDCNSLPGGLTCKETFNMYFESDENG- 166
QY 126 TFPNMENPVKVDITIAADSSFSQVDLGGVRVMTKINTVRSFVRSRSGFYLAQDYGCM 185
DB 167 --NIKQYIKIDITIAADEFTLGLDRVMTKINTVRSFVRSRSGFYLAQDYGACI 223
QY 186 SLIAVRVYRKCPRIQNGALFOETLSCAESTSIVAARGSCIANAEVDVPIKLYCNGDG 245
DB 224 ALVSVRVYKCPVVRHLAVFPDTITIGADSSQLLEVSGCV-NHSTDDPPKMHCSAEG 282

A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A38224; B38224
R:Wicks, I.P.; Wilkerson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A:Title: Molecular cloning of HEK the gene encoding a receptor tyrosine kinase expres
A:Reference number: A38224; MUID:92179233; PMID:1311845
A:Accession: A38224
A:Molecule type: mRNA
A:Residues: 1-983 <WIC>
A:Cross-references: UNIPROT:P29320; GB:M83941; NID:gl83931; PID:AAA58633.1; PID:gl83932
A:Experimental source: pre-B-cell leukemia cell line LK63
A:Note: sequence extracted from NCBI backbone (NCBI:86627)
A:Accession: B38224
A:Molecule type: protein
A:Residues: 21-39;810-860 <W12>
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F:542-565/Domain: transmembrane #status predicted <TM>
F:619-885/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:232,337,391,404,493/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 56.5%; Score 2930.5; DB 2; Length 983;
Best Local Similarity 57.0%; Pred. No. 1.1e-126;
Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

QY 20 EBTLMDSSTATAELGMMVHPSPGSEVSGVDENMTIRYQVCNVFSSQNNMLRTKPIR 79
DB 29 EYNLDSKTIQELGWIYSPGSEVSGVDENMTIRYQVCNVFSSQNNMLRTKPIR 88
QY 80 RGAHRIHVEMKFSVRDCSSIPSVPSCKETFNLYYYEADFDGATKIFPNWENPVKVD 139
DB 89 RSAOKIYVELFTLDCNSIPLVLTCTKEFNLYYEDDGHVK---PREHQFTKID 144
QY 140 TIAADESFQVDLGGVRVMTKINTVRSFVRSRSGFYLAQDYGCMVLIIVRYKCPR 199
DB 145 TIAADESFQVDLGGVRVMTKINTVRSFVRSRSGFYLAQDYGCMVLIIVRYKCPR 204
QY 200 ITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDCEMLVPIGRCMCKAG 259
DB 205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNNSEEDPP-RMYCSTEGEWLVPIGRKSCNAG 262
QY 260 FEAVENGTVRCGPGCTFRKQNDGDEACTHCPIINSRTTBEGATNCVCRNGYVRADLDPLDM 319
DB 263 YE--ERGFMCQACRPGFYKALDGNMKCAKCPHSSFTQEDGSMNCRNENYFRADKDPSPM 320
QY 320 PCTTIPSAQVITSSVNETSMLWTPPDSDGREDLVNIIKSCGSGRGACTRCGDNV 379
DB 321 ACTRPPSSPRNVISNINETSVIDLWSWPLDTGGRKDVTFNIIKCGKNWIKOCFCPSNV 380
QY 380 QYAPROGLTEPRIVISDLAHTQYTFEIOAVNGVTDQSPFQAFASVNIITNQAPSVA 439
DB 381 RFLPQPGLTNTVTVDLLAHNTYFEIDAVNGVSELSSPPRQFAAVSITTNQAPSVA 440
QY 440 SIHQVSRVSDSITLWSQPDQNGVILDELOYYEKSELSEYNATAKFTNTVTVQGLK 499
DB 441 LTIKQRTSRNLSISLWQDEHENGILDEVEYKQEQETSYTLTRAGNTVNTISL 500
QY 500 AGAIYVQVARTVAGRGYSGKMYFQTMTEASYQTSIQEKLPLITIGSSAAGLVFLIAYV 559
DB 501 PDTIYVQIIRARTAGGTNRKFEFTSPDS-FSISGESSQVMTAISAAVAIILLTV 559
QY 560 VIAIV---CNRGRPERADSEYTKLQHYTSGHM-TPGMKIYDPTFYEDPNEAVREFAKE 615
DB 560 IYVLIGRCFGYKSKHGAD---EKRLHFGNGLKLPGLRTYVDPHYEDPTQAVHFAKE 615
QY 616 IDISCVKIEQVIGAGEVCSGRLKLPKGRLEIFVAILKTLKSGVTEKQRDFLGEASIMG 675

mouse developmental kinase 2 (MDK2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148652
R:Clissek, T.; Lerch, M.M.; Ullrich, A.
Oncogene 11, 2085-2095, 1995
A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two novel members of the mitogen-activated protein kinase family
A:Reference number: 148652; MUID:96074837; PMID:7478528
A:Accession: 148652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-987 <RES>
A:Cross-references: UNIPROT:P54761; EMBL:Z49085; NID:g1089897; PIDN:CAA89909.1; PID:g1089897
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat domain
C:Keywords: ATP; transmembrane protein
F:322-417/Domain: fibronectin type III repeat homology <FN3A>
F:433-510/Domain: fibronectin type III repeat homology <FN3B>
F:613-881/Domain: protein kinase homology <KIN>
F:621-629/Region: protein kinase ATP-binding motif
F:904-970/Domain: SAM homology <SAM>

Query Match 55.0%; Score 2854.5; DB 2; Length 987;
Best Local Similarity 56.4%; Pred. No. 3.2e-123;
Matches 552; Conservative 159; Mismatches 251; Indels 17; Gaps 10;

QY 6 LGAAALLPILAAVEETLMDSTTATAELGVMVHPSP--GWEVSGYDENMNTIRTYOVCN 63
DB 3 LRAILCWASLATALEETLNTKLETLKWTYTPQAEQWEEELSGLEDEHSHVRYTEVCD 62
QY 64 VPE-SSQNNWLTKEFIRRGGAHRHVENKFSVRDCSSIPSPVSGCKETFLNLYYEADFD 122
DB 63 MKRPGQGAHLURKTGWPRGAVHVATIRFTMECLSLPRASRSCKETFTVFYIESERT 122
QY 123 AKTTPFNWMMENPWVKVDITIADESPSQVDLGRVNMKINTEVRSFGPVSRSQFYLAPODG 182
DB 123 ATAHTPAMWENFYIKVDITVAEHLTRKPRGAETGKVNKIKTLRLGLPSKAGFYLAPODG 182
QY 183 GMSLIAVRFYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPI-KLYC 241
DB 183 ACWALLSLFKYKCSWLITNTYTFEIV---PRELVFVAGSCVANAAPVTPANSPSLYC 239
QY 242 NGDGWL-VPIGRCKMCKAGFAVNGTVCRGCPSTFKANQDEACTHCPINSTRTEGA 300
DB 240 REDGQWAEQVTCSCAPGFAEAEKVKCRACGQGTFFQIGDESLPCPANSHNNGS 299
QY 301 TNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNI 360
DB 300 PVCLCRIGYRARSDDPRSFCTTPPSAPRSVHHLNGSTLRLEWAPLESQGLDLYAV 359
QY 361 ICKSCGSGRGACTRCGDNVQYAPRQLGLTEPRIVYSDLLAHTQYTFEIQAVNGVTDQSPF 420
DB 360 RCRCRPG-GSCLPCQGDWTFPGPRDLVEPVAIRGLRDPVYTFEVAALNGVSTLATG 418
QY 421 SPQFASVNIITNOAAPSAVSIHMQVSRVDSITLWSQDPQNGVILDYELQYKEKLS 480
DB 419 PPPEPVNITDREVPAVSDIRVTRSSPSLISWAIAPRAGSAVLDEYVKYHKGAG 478
QY 481 YNATA-IKSTNTVTVQGLKAGAIYVQVARTVAGYGRYSQVMYFQT-MTEARYQTSIQ 538
DB 479 PSSVRFLKTSNRAELRGLRGASYLIVQVRASEAGYGPQGHSHSQTLQDSE---SWR 535
QY 539 EKLPLIIGSAAAGFLVIAVVIIVCNRRGRFERADSEYTDKLOHYTSQHMTPGKMIYID 598
DB 536 EQALLAGTAVGVVLVVLVVLVIAVLCLRKQSGREVEYSDKHGQVLIH---GTRKVYID 592
QY 599 PFTYEDNEAVREFAKEIDISCVKIQVITGAGFEGVCSCHLKLPGKREIFVAIKLXSG 658
DB 593 PFTYEDNEAVREFAKEIDISYVKIEVIGAGFEGVCRGLKAPAKKSSCAVAILKXG 652
QY 659 YTEQRDFLSEASIMQFQHPNVHLEGVTVTKSTFVMIITEFMENGLSDSLRQNDQGF 718
DB 653 YTEQRDFLSEASIMQFQHPNIIIRLEGVTVNSVFMILTEFMENGLSDSLRQNDQGF 712

QY 719 TVIQVGLRGIAAGMKYLDAMNVTYHRDLAARNILVNSLVCKVSDPGLSRFLEDDTSDP 778
DB 713 TVIQVGLRGIAAGMKYLAEMSVYHRDLAARNILVNSLVCKVSDPGLSRFLEENSSDP 772
QY 779 TYSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIYVWVMSYGERPYWDMNQDVINA 838
DB 773 TYSALGGKISIRWTAPEAIQYRKFTSASDAWSYGIYVWVMSYGERPYWDMNQDVINA 832
QY 839 IEQDYELPPMDPCSAHQMLDCQKDRNHRPKFGQIVNTLDKWIENPNSLKAMAPLSS 898
DB 833 IEQDYELPPMDPCSAHQMLDCQKDRNHRPKFGQIVNTLDKWIENPNSLKAMAPLSS 892
QY 899 GINPLDRTIDPTYSFNTVDENLEAIKMGQYKESPANAGTSDVDVVSQMMEDILRGV 958
DB 893 GASHELLDQRPYSAFGSVGEWLRKMGVYEEBFAAGFSGFEVVSQISAEEDLLRIGV 952
QY 959 TLAGHOKILINSIQVMRAQ 977
DB 953 TLAGHOKILASVQHMKSQ 971

RESULT 23
AS4092
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: AS4092
R:Bennett, B.D.; Wang, Z.; Kuang, W.J.; Wang, A.; Groopman, J.E.; Goeddel, D.V.; Scadden
J. Biol. Chem. 269, 14211-14218, 1994
A:Title: Cloning and characterization of HTK, a novel transmembrane tyrosine kinase of the
A:Reference number: AS4092; MUID:94245746; PMID:8188704
A:Accession: AS4092
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-987 <BEN>
A:Cross-references: UNIPROT:P54760; GB:U07695
C:Genetics:
A:Gene: GDB:HTK
A:Cross-references: GDB:362753; OMIM:600011
A:Map position: 7pter-7qter
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat domain
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase
F:433-518/Domain: fibronectin type III repeat homology <3FR>
F:613-881/Domain: protein kinase homology <KIN>
F:621-629/Region: protein kinase ATP-binding motif
F:904-970/Domain: SAM homology <SAM>

Query Match 54.8%; Score 2844; DB 2; Length 987;
Best Local Similarity 56.0%; Pred. No. 9.5e-123;
Matches 553; Conservative 160; Mismatches 247; Indels 28; Gaps 13;

QY 1 MALRRGAALLPILAAVEETLMDSTTATAELGVMVHP--PSGWEVSGYDENMNTIR 58
DB 1 MELRVL---LCWASLATALEETLNTKLETLKWTYTFEIVQVDGQWEEELSGLEDEHSHV 57
QY 59 YQVNCVPE-SQNNWLTKEFIRRGGAHRHVENKFSVRDCSSIPSPVSGCKETFLNLYYE 117
DB 58 YEVCDVQAPQAEHLTKGWPRGAVHVATIRFTMECLSLPRASRSCKETFTVFYIE 117
QY 118 ADFDSATKTPFNWMMENPWVKVDITIADESPSQVDLGRVNMKINTEVRSFGPVSRSQFYLA 177
DB 118 SDADTATALTAPWMMENFYIKVDITVAEHLTRKPRGAETGKVNKIKTLRLGLPSKAGFYLA 177
QY 178 FQDYGGMCSLIAVRFYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPI 237
DB 178 FQDYGGMCSLIAVRFYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPI 234
QY 238 -KLYCNGDGWL-VPIGRCKMCKAGFAVNGTVCRGCPSTFKANQDEACTHCPINSTR 295
DB 235 PSLYCREDGQWAEQVTCSCAPGFAEAEKVKCRACQGTFFPLSGEGSCQPCPANSHS 294
QY 296 TSEGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGRED 355
DB 296 TSEGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGRED 355

Db 295 NTIGSAVQCVRGVGFARTDPRGAPCTTPPSAPRSVVRSLNGSLHLLEWGAPELSSGGRED 354
Qy 356 LVNINICKSGRGACTCGDNVQYAPROGLGTEPRIYISDLAHTQYTFEIQVANGV- 414
Db 355 LTVALRCRCRPG-GSCAPCGDLTPDGPDLVPEVWVVRGLRPDFTYTFEVALNGVS 413
Qy 415 ---TDGPPFPQFASVNTTNAAPSASVIMHQVSRVTDITISWSQDPQNGVILDYEL 471
Db 414 SLATGPVPFEP---VNVVTTDREVPAVSDIRVTRSSPSSLAWAVPRAPSGAVLDYEV 469
Qy 472 QYVEKELSEYNATA- IKSPTNTVTVOGLKAGAIYVFOVARTVAGYGRYSKGYFOT-MT 529
Db 470 KYHEKGAEGSSVRFLKTSNRARLGLKRGASTLVQVARSAGYFPFQOEHSQTOLD 529
Qy 530 EAEYQTSIQEKLPLIIGSSAAGLVFLIAVAVIAVCNRRGFERADSEYTDKLOHYTSGHM 589
Db 530 ESE---GWRQLALIACTAVVGVVLVAVVAVLCLRKQSGREAEYSKDGQYLLGH- 585
Qy 590 TPGMKYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 649
Db 586 --GTVKVIDPFTYEDPNEAVREFAKEIDVSVYKIEEVIGAGEFGEVCRGLKAPGKKEC 643
Qy 650 VAIKTLKSGYTEKORRDFLSEASTMGOFDHPNVHLGVVTKSTPYMIITEFMENGLSDS 709
Db 644 VAIKTLKGGYTEKORRDFLSEASTMGOFDHPNIIIRLGVTNSMPVMIITEFMENGALDS 703
Qy 710 FLRQNDGQFTVIOLVGMLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSR 769
Db 704 FLRLNDGQFTVIOLVGMLRGIAAGMYLAEMSYYHRDLAARNILVNSLVCKYSDFGLSR 763
Qy 770 FLEDDTSDPTYSALGKGKIPIRWTAPAIQYRKPTASDVWSYGIWVMEVMSYGERPYWD 829
Db 764 FLEENSSDPTYSALGKGKIPIRWTAPAIQYRKPTASDVWSYGIWVMEVMSYGERPYWD 823
Qy 830 MTNQDVINAEDYRLPPPPWDCSALHOLMDCWKDRNHRPKRGQIVNTLDKWRNPNS 889
Db 824 MSNQDVINAEDYRLPPPPWDCSALHOLMDCWKDRNHRPKRGQIVNTLDKWRNPAS 883
Qy 890 LKAMAPLSSGINPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMM 949
Db 884 LKIVARENGASHPDLLDQRPYSAFSGVGEWLAIRKMGYRESFAAAGFSGFELVSQIS 943
Qy 950 MEDILRGVTLAGHQKILNSIQVMAQ 977
Db 944 AEDLLRIGVTLAGHQKILASVQHMKSQ 971

RESULT 24
148953
eph-related receptor protein tyrosine kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48953
R;Andres, A.C.; Reid, H.H.; Zurcher, G.; Blaschke, R.J.; Albrecht, D.; Ziemiacki, A.
Oncogene 9, 1461-1467, 1994
A;Title: Expression of two novel eph-related receptor protein tyrosine kinases in mammary
A;Reference number: I48953; MUID:94203677; PMID:8152808
A;Accession: I48953
A;Status: preliminary; translated from GH/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-987 <RES>
C;Cross-references: UNIPROT:P54761; EMBL:U06834; NID:9459172; PIDN:AAAI8591.1; PID:94591
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
F;322-417/Domain: fibronectin type III repeat homology <FN3A>
F;433-518/Domain: fibronectin type III repeat homology <FN3B>
F;613-881/Domain: protein kinase homology <KIN>
F;621-629/Region: protein kinase ATP-binding motif
F;904-970/Domain: SAM homology <SAM>

Query Match 54.2%; Score 2811.5; DB 2; Length 987;
Best Local Similarity 55.8%; Pred. No. 2.9e-121;
Matches 545; Conservative 159; Mismatches 256; Indels 17; Gaps 10;

Qy 6 LGAALLPLLAAVEETLMDSTTATAELGWNVHPPS--GWEEVSGYDENNMNTRTYQVCN 63
Db 3 LRALLCWASLATALEETLLNTKLETADLKWVTPYQAEGQWEELSGLEEQHSVRYTEVCD 62
Qy 64 VFE-SSONNWLRTKTRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKTFLNLYYEADPDS 122
Db 63 MKRPGGQHLWLRGTGWPRRGAVHYATIRFTMCECLSPRASRSCKETFTVFYYESRDT 122
Qy 123 ATKTFENNMENPMVKVDTIAADESFQVDLGGVRMKINTVRSFGVPSRSGFYLAFOGY 182
Db 123 ATAHTFAMMENPMVKVDTVAEHLTRKPGAEATGKVNIIKTLRGLPUSKAGFYLAFOQG 182
Qy 183 GCMSLIAVRVYFKCPRIIQNGAIFOBTLGSAESTSLVAARGSCIANAEVDPFI-KLYC 241
Db 183 ACWALLSLHLFYKCSWLIITNLTYFPETV--PRELVVPVAGSCVANAAPTANPSPLYC 239
Qy 242 NGDGEWL-VPIGRCMCKAGFEAVENGTVCRGCSPTGTFKANQGDCACTHCINSRTTSEGA 300
Db 240 REDGQWABQQVTCSCAPGYEAAESNKKVCRACQGTGPKQIGDESCCLPCPANSNNIGS 299
Qy 301 TNCVCRNGYYRADLDPLDMPCCTTIPSAPOAVISSVNETSLMELWTPRPDSGGRDLVYNI 360
Db 300 PVCLCRIGYTRASDRSPSPCTTPPSAPRSVVHHLNGSTLRLWSAPLESGRPDLYAV 359
Qy 361 ICKSCSGRGACTCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIQVANGVTDQSPF 420
Db 360 RCRCRPG-GSCLPCGDMTDFGPRDLVERWVAIRGLRPDVTYTFEVAALNGVSTLATG 418
Qy 421 SPOFASVNTTNAQASVIMHQVSRVTDITISWSQDPQNGVILDYELQYKEKELSE 480
Db 419 PPPFPVNVTTDREVPAVSDIRVTRSSPSSLISWAIAPRAPSGAVLDYEVKYEKGAEG 478
Qy 481 YNATA-IKSPNTVTVOGLKAGAIYVFOVARTVAGYGRYSKGYFOT-MTEABYQTSIQ 538
Db 479 PSSVRLKTSNRARLGLKRGASTLVQVARSAGYFPFQOEHSQTOLDSE--SWR 535
Qy 539 EKLPLIIGSAAAGLVFLIAVAVIAVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYID 598
Db 536 EQALAGTAGVAVGVVLVAVVIAVLCLRKQSGREVEYSDKHQYLLGH--GTVKYID 592
Qy 599 PFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTKSG 658
Db 593 PFTYEDPNEAVREFAKEIDVSVYKIEBEVIGAGEFGEVCRGLKAPGKKECVAIKTKSG 652
Qy 659 YTEKORRDFLSEASTMGOFDHPNVHLGVVTKSTPYMIITEFMENGLSDSFLRNDGQF 718
Db 653 YTERQRAEFLEASIMGQFEPHNIIRLEGVVTNSVPVMIITEFMENGLSDSFLRNDGQF 712
Qy 719 TVIQLVGLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSRFLDDTSDP 778
Db 713 TVIQLVGLRGIAAGMYLAEMSYYHRDLAARNILVNSLVCKYSDFGLSRFLDENSDP 772
Qy 779 TYTSALGKGKIPIRWTAPAIQYRKPTASDVWSYGIWVMEVMSYGERPYDMTNDVINA 838
Db 773 TYTSALGKGKIPIRWTAPAIQYRKPTASDVWSYGIWVMEVMSYGERPYDMTNDVINA 832
Qy 839 IEODYRLPPMDPCPSALHOLMDCWKDRNHRPKGQIVNTLDKWRNPNSLKAMAPLSS 898
Db 833 IEODYRLPPMDPCPSALHOLMDCWKDRNHRPKGQIVNTLDKWRNPNSLKAMAPLSS 892
Qy 899 GINPLPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRGV 958
Db 893 GASHPLLDQRPYSAFSGVVEWLAIRKMGYRESFAAAGFSGFEMYSQISAEADLLAIGV 952
Qy 959 TLAGHQKILNSIQVMAQ 975
Db 953 TLAGHQKILASVQHMKSQ 969

RESULT 25
150617
protein-tyrosine kinase (EC 2.7.1.112) Cek8 - chicken (fragment)

C;Species: Gallus gallus (chicken)		
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004		
C;Accession: I50617; S33505		
R;Sajjadi, F.G.; Pasquale, E.B.		
Oncogene 8, 1807-1813, 1993		
A;Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.		
A;Reference number: I50611; MUID:93288394; PMID:8510926		
A;Accession: I50617		
A;Status: preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type: mRNA		
A;Residues: 1-849 <SAJ>		
A;Cross-references: UNIPROT:Q07496; EMBL:Z19059; NID:g312216; PID:g3122		
C;Genetics:		
A;Gene: Cdk8		
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h		
C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki		
F;482-748/Domain: protein kinase homology <KIN>		
F;490-498/Region: protein kinase ATP-binding motif		
F;771-837/Domain: SAM homology <SAM>		
Query Match 52.6%; Score 2728.5; DB 2; Length 849;		
Best Local Similarity 59.6%; Pred. No. 1.5e-117;		
Matches 512; Conservative 139; Mismatches 181; Indels 27; Gaps 9;		
Qy	132 ENPWKVDTTAADSFSQVDLGRVWKINTEVRSFGVSRSGFYLAPODYGGWLSIAVR	191
Db	2 ESQPAKIDTTAADSFTQVDIGDRIMKLNTEVDRVGLSKKGFYLAPODYGGACIALVSVR	61
Qy	192 VFYRKCPRIQNGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYNGDGEWLVI	251
Db	62 VFYKCPILVNLAQFPDITGATSSLVVRGSCVANSSEKVP-KWYCGADGEWLVI	120
Qy	252 GRMCKAGFAVENGTVCRCPSFTFKANQDEACTHCIPNSTRTSAGTNCVCRNGYR	311
Db	121 GNCLNAGYE--ERNGEQACKIGYKALSTDVACAKCPHSHSYISWEGSTCTCDRFFR	178
Qy	312 ADLPLDMPCCTIPSAQAVLSVNETSLMLEWTPPRDSGGREDLVNIIICKSCGSGRGA	371
Db	179 AENDASMPCTRPPSAPQLISNNVETSVNLENAPQNKGRDDISVNVCKRCGAGEPS	238
Qy	372 -CTRGGDNVQAPROGLTEPRIYISDLLAHTQYTFEIQAVNGVDQSPSPQASVNI	430
Db	239 HCRSGSGVHFSPQNGKLTTKVSTIDLLAHTNTFEVWAVNGVSKNPSQDQAVSVT	298
Qy	431 TNQAAPSASVIMHQVSRVDSITLSWSQDPQNGVLDLYELQYKEKELSEYNATAIKSPT	490
Db	299 TNQAAPSPALTOAKEITRHSVALAWLEDPNGVILEYKYEKQONERTYRIVKIAS	358
Qy	491 NTVTVQGLKAGAIYVQVRAITVAGYGRYSGMYFQMTAEAYQTSIQEKL-----PLI	544
Db	359 RNTDINGLNLPLTSYVPHVRAITAAGYGFSGPFETNT-----VPSPIIGDTNPTV	411
Qy	545 IGSSAAGLVFLIAVVVIAVNCNR--GPERADSEVTDKLQHTSGHMTGPKMIYIDPTY	602
Db	412 LLVSVAGSVLVVLIIAIAFVSRRSKYSKAKQEADEE-----KHLNQGVRTYVDPTY	465
Qy	603 EDPNFAVREFAKEIDISCKVEQVIGAGEFGVCSGHLKPGKRIFFVAIKTLKSGYTEK	662
Db	466 EDPNQAVREFAKEIDASCIIKEKVIGVGEFGVCSGRLLKVPKREICVAIKTLKAGYDK	525
Qy	663 QRDRFLSEASIMQDPDHPNVHLEGVVTKSTPMIITEFMNGSLDSFLRQNDGQFTVIQ	722
Db	526 QRDRFLSEASIMQDPDHPNI IHLEGVVTCKPVMIIITEFMNGSLDAFLRKNDRFTVIQ	585
Qy	723 LVGMURGIAAGKYLADMYVHRDLAARNILVNSLVCKVSDPGLSRFLEDDTSPDPTS	782
Db	586 LVGMURGISGKMYLSDMSYVHRDLAARNILVNSLVCKVSDPFGMSRVLEDD--PRAATY	644
Qy	783 ALGGKIPITWTAPEAIQYRKFTSASDVWSYGIWVMEVMSYGERPYWDMTNQDVINAIED	842
Db	645 R-GGKIPITWTAPEAIYRKFTSASDVWSYGIWVMEVMSYGERPYWDMNSQDVKAIEEG	703
Qy	843 YRLPPPMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMTNPNLSLKAMAPLSGGINL	902

Db	704 YRLPPPMDCPTALHQLMDCWQKERSDRPKFGQIVNMMLDLIRNPNLSIKRTGSSSRPST	763
Qy	903 PLLDRTIPDYSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVLAG	962
Db	764 ALLOPSSPEFSAVSVSWDLQAIKMYRYKDNFTAGTYTLEAVVHMNQDDLARIGITAIT	823
Qy	963 HOKKILNSIQVWRAQMNQI	981
Db	824 HONKILSSVQAMRSQMQM	842
RESULT 26		
S51605		
receptor-like tyrosine kinase Etk-2 - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004		
C;Accession: S51605		
R;Maisonnier, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.		
Oncogene 8, 3277-3288, 1993		
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam		
A;Reference number: S49015; MUID:94067777; PMID:7504232		
A;Accession: S51605		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-948 <MAI>		
A;Cross-references: UNIPROT:P54758; EMBL:S68030		
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h		
C;Keywords: ATP; transmembrane protein		
F;628-936/Domain: protein kinase homology <KIN>		
F;636-644/Region: protein kinase ATP-binding motif		
Query Match 50.1%; Score 2599.5; DB 2; Length 948;		
Best Local Similarity 53.1%; Pred. No. 1.3e-111;		
Matches 498; Conservative 147; Mismatches 225; Indels 67; Gaps 12;		
Qy	13 LPILAA-----VEETLMDSTATAELGHWVPPSGWEVSGYDENMNTIRTYQVCN	63
Db	17 LPILLTAWTGDCSHVSNQVLLDTSTVMGELGWKTYPLNGWDATTEMDEHNRRIHTYQVCN	76
Qy	64 VFSSQNNMLRTKFIERRGAHRIHVEMKFSVRDCSPVSGSCKETFLNYEADFSA	123
Db	77 VMEPNQNNMLRTNWSRDAQAQIYVEMKFTLRDCNSIPWVLGTCKETFTLYIESDESHG	136
Qy	124 TKTFPNNMENPWKVDITIAADSFSQVDLGRVWKINTEVRSFGVSRSGFYLAPODYGG	183
Db	137 TKFKP---SQYKIDTIAADESFTQMDLGRILKLNTEVREVGPIERKGFYLAPODIGA	192
Qy	184 CMSLIAVRVYRCPRIQNGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYCNG	243
Db	193 CIALSVRVYRCKPFTVRNLAMPDTIIPRVDSLSLVEVRGSCVKSEERDTP-KLYCGA	251
Qy	244 DGMWLVPIGRMCKAGFAVENGTVCRCPSFTFKANQDEACTHCIPNSTRTSSEGTATNC	303
Db	252 DGMWLVPLGRCICTTGVEELEG--CHACKPGYKAPAGNTKCKCPHSHSTFEATSV	309
Qy	304 VCRNGYVRADLDPLDMPCCTIPSAQAVLSVNETSLMLEWTPPRDSGGREDLVNIIICK	363
Db	310 HCEKGYFAEKDPPSACTPPSAPRNVAFINETALILEWSPSDTGGRKRDUTYSVICK	369
Qy	364 SCGSGRACRCGDNVQVAPRQLGTEPRIYISDLLAHTQYTFEIQAVNGVDQSPSPQ	423
Db	370 KCGVDASQCRDCCAGLAFIPRPTGLINNVSVVLDVFSHVNYTTEIEMNGVSELSIPKP	429
Qy	424 FASVNTTNOAPSASVIMHQVSRVDSITLSWSQDPQNGVLDLYELQYKEKELSE--Y	481
Db	430 FTAITVTDDQAPSLIGMRKDWASQNSLALSQAFAFNGAIDLYEIKYEKEHEULTY	489
Qy	482 NATAIKSPFTVTVQGLKAGAIYVQVRAITVAGYGRYSGMYFQMTAEAYQTSIQEKL	541
Db	490 SSTSKAP--SVIITGLKPDATTYFIHVRVTAITGYSGYSOKFFETGDETSDMAEQGI	547
Qy	542 PLIIGSSAAGLVFLIAVVVIAVNCNR-RGPERADSEVTDKLO-HYTSGHMT-PGMKIYID	598

548 LVIATAAVGGFTLLAVLTLPFLITGRQWYIKAKMKSEKRTHLQNSHLRFPQIKTYID 607
599 PFTVEDNEAREFAKIDISCVKIEQVIGAGEGVCSEGLKLPGRKEIFVAITKLSG 658
608 PDTVEDSLAHEFEKIDPSRIERIVIGAGEGVCSEGLKTPGRKEIPVAITKLSG 667
659 YTEKQRDFLEASIMQGFQHPNVHLEGVVTKST----- 693
668 HMDQRDFLEASIMQGFQHPNIIRLEGVVTKESEFPALGVEAFPCPSFLRAGFLNGIQAP 727
694 -----PVMITFEMENGLSDSFLRQNDQGFVQLVGLMGLRTAGAKMY 736
728 HPVTAGGSLPPRIAPGRPMVIMWEYMGNSLDSFLRKHDGHTFVQLVGLMGLRTAGAKMY 787
737 LADNMVVRDLAARNILVNSLVCKVDFGLSRFLEDDTPTYSALGGKIPRWTAP 796
788 LSDMGVVRDLAARNILVNSLVCKVDFGLSRFLEDD-PEAAVTTT-GGKIPRWTAP 845
797 AIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINAIRQDYRLPPMDPCPSALH 856
846 AIAYRKFSASDVMSYGIWMEVMSYGERPYWMSNQDVILLISIEGYRLPAPMCPSPSLH 905
857 QLMLDCKQKRNHRPKFGQIVNTLDKMRNPNSLKAM 893
906 QLMHLCHQKRNHRPKFTDIVSFLDKLRNPSSALHTL 942

RESULT 27
S47489
receptor tyrosine kinase - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S47489
R:Taylor, V.; Pfaff, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lessmann, H.; Sch
submitted to the EMBL Data Library, April 1994
A:Description: Expression and developmental regulation of EHK-1, a neuronal ELK-like rec
A:Reference number: S47489
A:Accession: S47489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-898 <TAY>
A:Cross-references: EMBL:X78689; NID:G531543; PIDN:CAA55357.1; PID:G531544
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
P:568-834/Domain: protein kinase homology <KIN>
P:576-584/Region: protein kinase ATP-binding motif

Query Match 48.8%; Score 2531; DB 2; Length 898;
Best Local Similarity 51.0%; Pred. No. 1.7e-108;
Matches 495; Conservative 142; Mismatches 185; Indels 148; Gaps 13;

QY 6 LGALLLLPILAAVEETLMDSTTATBLGVMVHPSPGWEESGVGYDENWNTIRTYQVCNVP 65
DB 53 LCAALRTLLASPSNEVLLDSRTVLGDLGTAFFKNGWEIEGYDENYAPHTYQVCNVM 112
QY 66 ESSQNNWLRTKFRIRRGAAHRTHVEMKFSVRDCSSIPSPVSGKETFNLVYEAADFDSATK 125
DB 113 EQQNNWLLTSWISNEGASRIFELKFTLRDCNLSLPGGLGTCKETFMVYFESDENGR- 171
QY 126 TFPNMENPMVKVDITIAADESFSQVDLGGVRVMKINTEVRSFVPSRSGFYLAFOYGGCM 185
DB 172 ---NIKENQYIKIDTIAADESFTLDDLRVWMLNTEVRDVGPLSKGKGFYLAFOVGACI 228
QY 186 SLIAVRPYRKCPRIQNGAIFQTLGSAETSLVAARGSCIANAEVDVPILKLYCNGDG 245
DB 229 ALVSRVRYKKCPGVRHLAVFPDITIGADSSQLLEVSGSCV-NHSTVDDPPPKHCSAEG 287
QY 246 EWLVPICRMCKACGAFAVENGTCVRCGPGSGFFKAGQDGAECTHCPINSTRITSECATNCVC 305
DB 288 EWLVPICRMCKACGAFAE-KNKT-CQVCRPGFKASPHISQTCCKPSPHYTHEEASTSCVC 345
QY 306 RNGYYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTTPRDRSGGREDLVVNIICKSC 365

346 EKDYFRRESDPPTMACTT----- 363
366 GSGRGACTRGDNQVAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPSPQFA 425
364 ----- 363
426 SVNITNQAAAPSASVIMHOVSRTVDSITLSWSQDPQNGVILDYELQYKELSEYNATA 485
364 -----PSPVTNVKKGKIAKNSISLSQBPDPENGILLEYEIKYFEKD-QETSVTI 412
486 IKSPFTNTVTVQGLKAGAIYQVQVARTVAGYGRYSKMYFQMTTEASYQISIQKFLPII 545
413 IKSKETITITAEGLKPAVVYVQIRARTAAAGYGVFSRFEFET-TPVFAASNDQSQIPIIA 471
546 GSSAAGLVFLIAVVVTAIV-----CNRR-----GFERADSSYTTDKLQ 582
472 VSVTVG-VILLAVNIGFLLSGCCGCCGRASSLCAVAHPSLIWRCYSKAKQDPPEEKM 530
583 HYTSGHM-TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLK 641
531 HFHNGHIKLPVRTYIDPHTYEDPTQAVHEFAKEIEASCITIERVIGAGEFGEVCSGRLK 590
642 LPKREIFVAIKTLKSGYTEKQRDFLSEASIMQGFQHPNVHLEGVVTKSTPMITTEP 701
591 LPKRELPFAIKTLKVGYTEKQRDFLSEASIMQGFQHPNIIHLEGVVTKSKPMIVTEY 650
702 MENGSLDSPURONDQFTVQLVGLMGLRTAGAKMYLADNMVVRDLAARNILVNSLVCK 761
651 MENGSLDTFLKQNDQFTVQLVGLMGLRTAGAKMYLSDMGVVRDLAARNILVNSLVCK 710
762 VSDPGLSRFLEDDTPTYSALGGKIPRWTAPAIQYRKFTSASDVMSYGIWMEVMS 821
711 VSDPGLSRFLEDD-PEAAVTTT-GGKIPRWTAPAIQYRKFTSASDVMSYGIWMEVMS 768
822 YGERPYWDMNQDVINAIRQDYRLPPMDPCPSALHQLMDCWQKDRHHRPKFGQIVNTLD 881
769 YGERPYWDMNQDVINAKAVEEGYRLPSPMDCPAALYQLMDCWQKDRHHRPKFGQIVNTLD 828
882 KMIARNPSLKAMAPLSSGINPLDRTIPDYTSFNTVDEWLEAIKMGQYKESPANAGTTS 941
829 KLIRNPSSLTKLVNASSRVSTLLAEHSGSLSGAVRSVGEWLEAIKMGRYTEIFENGYSS 888
942 FDVVSQMMME 951
889 MDAVAQVTL 898

RESULT 28

S51603

receptor-like tyrosine kinase Ehk-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S51603

R:Malsonptierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A:Title: EHK-1 and EHK-2: two novel members of the Eph receptor-like tyrosine kinase fam

A:Reference number: S49015; MUID:9406777; PMID:7504232

A:Accession: S51603

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-893 <MAI>

A:Cross-references: UNIPROT:P54757; EMBL:S68028

A:Note: the authors translated the codon GAC for residue 170 as Glu

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C:Keywords: ATP; transmembrane protein

P:563-829/Domain: protein kinase homology <KIN>

P:571-579/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 48.4%; Score 2512; DB 2; Length 893;

Matches 492; Conservative 142; Mismatches 188; Indels 148; Gaps 13;

Qy	6	LGRAALLPLLA	VEETLMDSTATAELGHWVHPSPGSEVSGYDENMNTIRTYQYCNVF	65
Db	48	LCAALRTLLAS	PSNEVNLDSRTVLGDLGWIAFPKNGWEEIGEVNDENYAPIHTYQCKWM	107
Qy	66	ESSQNNWLRTK	FTRRRGARHIHVEMKFSVRDCSIPSPGSCKETENLNYEAFDPSATK	125
Db	108	EQONQNWLLIS	WISNEGASRIFIELKETLADCNLSLPGGLGTCKETFNMYFESDDENGR	166
Qy	126	TFPNMNMNPM	VKVDITIAADSFQVDLGGVRMKINTEVRSGFVLAQDYGGCM	185
Db	167	---	NIKNQVTKIDTIAADESFTELDLGDVRMKLNTETVRDVGPLSKGFGYLAQDYGACI	223
Qy	186	SLIAVRFYRK	CPRIIQNGAIFORTLSGAESTSIVAARGSCIANAEVDVPIKLYCNGDG	245
Db	224	ALVSRVYYKK	CPVSRVHLAVPDTITGADSSQLLEVSGCV_NHVSVDTPPKWHSAGC	282
Qy	246	EWLVPICRCM	KAGFAVENGTVCRCGPGSGTFFKANQGDDEACTHCPINSRTTSGATNCVC	305
Db	283	EWLVPICMKC	KAGYEB_KNGT-CQVCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVC	340
Qy	306	RNGYIRADLD	PLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVNIIKSC	365
Db	341	EKDYFRRES	DPPTMACTT-----	358
Qy	366	GSGRGAC	TRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPFSPQFA	425
Db	359	---	-----	358
Qy	426	SVNITNQAP	SAYSIMHQVSRTVDSITLWSQDPQNGVILDVLEYKKEISEYNATA	485
Db	359	---	-----	407
Qy	486	IKSPNTVTVO	GLKAGALVPOVPAARTVAGVGRYSGKMYQTMTAEAYQTSIQEKLPLII	545
Db	408	IKSKETTIT	AEGLKPAVSIVVFQIRARTAAAGYVFSRRPEPET-TPVFGASNDQOIP-II	465
Qy	546	GSSAAGLVFL	IAVVVIAIV-----CNRR-----	582
Db	466	GVSVTGVIL	LAVMIGFLLSGCCCGGRASSLCAVAHPSLIWRGYSKAKQDPBEKYM	525
Qy	583	HYTGSHM-	TPGMKIYIDPFTVEDNEAVREPAKIDISCVKIQVIGAGFGEVCSGHLK	641
Db	526	HFHNGHIK	LPGRVTVIDPHTYEDPTQAVHEFGKEIEASCITIERVIGAGEFGEVCSGRLK	585
Qy	642	LPGRKEIFVA	IKTLKSGYTEKQRDFLSEASIMQGDHPNVIHLEGGVVTKSTPVMIIIEF	701
Db	586	LPGRKEIPVA	TKLKVGTEKQRDFLSEASIMQGDHPNVIHLEGGVVTKSKPVMIIIEY	645
Qy	702	MENGLSDS	FLRQNDGQFTVIQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSLVCK	761
Db	646	MENGLSDT	FLKNDGQFTVIQLVGMRLGIAAGMKYLSDMGVYVHRDLAARNILVNSLVCK	705
Qy	762	VSDFLG	FLRLEDDTSDPTYSNAGKGIPIRTAPEAIQYRKFTSASDVWSYGIWVWEVMS	821
Db	706	VSDFLG	SLVLEDD-PEAYTTR-GGKIPIRTAPEAIAFRKFTSASDVWSYGIWVWEVVS	763
Qy	822	YGERPYW	DMTNDQVINAIEQDYRLPPPMDCPSALHQLMDCQKDRNHRPFGQIVNTLD	881
Db	764	YGERPYW	MTNQDVIAKAVEGYRLPSPMDCPAALVQLMDCQKDRNSRPKFDVIVNMLD	823
Qy	882	KMIRNP	NSLKAWAPLSSGINLPLLDRTIPDYTSFNTVDEWLEAKMGQYKSPANAGTS	941
Db	824	KLIRNP	SSLKTLVNASSRVTLLAEHSGLSGAYRSVGWELEATKMGRYTEIFPMENGYSS	883
Qy	942	FDVVSQ	MMME 951	
Db	884	MDAVAQ	VTLLE 893	

RESULT 29
A57174
protein-tyrosine kinase (EC 2.7.1.112) erk - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 05-Jan-1996 #sequence revision 05-Jan-1996 #text_change 09-Jul-2004
C/Accession: A57174; S23362; S40294; PN0547
R/Saio, T.; Seki, N.; Matsuda, Y.; Kitahara, M.; Murata, M.; Kanda, N.; Nomura, N.; Yamagomics 26, 382-384, 1995
A/Title: Identification of the human ERK gene as a putative receptor tyrosine kinase and A/Reference number: A57174; MUID:95324932; PMID:7601466
A/Accession: A57174
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-478 <SAI>
A/Cross-references: UNIPROT:P29323; GB:D37827; NID:g1060894; PIDN:BAA07073.1; PID:g1060894
Oncogene 6, 1057-1061, 1991
A/Title: erk and erk, new members of the eph subclass of receptor protein-tyrosine kinases A/Reference number: S23361; MUID:91296384; PMID:1648701
A/Accession: S23362
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 144-154, 'N', 156-204 <CHA>
A/Cross-references: EMBL:X59292
R/Watt, V.M.
submitted to the EMBL Data Library, May 1991
A/Reference number: S40294
A/Accession: S40294
A/Molecule type: mRNA
A/Residues: 144-204 <WAT>
A/Cross-references: EMBL:X59292; NID:g31222; PIDN:CAA41981.1; PID:g312223
R/Iwase, T.; Tanaka, M.; Suzuki, K.; Naito, Y.; Sugimura, H.; Kino, I.
Biochem. Biophys. Res. Commun. 194, 698-705, 1993
A/Title: Identification of protein-tyrosine kinase genes preferentially expressed in embryo A/Reference number: PN0547; MUID:93343925; PMID:7688222
A/Accession: PN0547
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 132-162, 'R', 164-478, 'X' <IWA>
A/Cross-references: DDBJ:D14717
C/Genetics:
A/Gene: GDB:ERK
A/Cross-references: GDB:128637; OMIM:176946
A/Map position: 1p36.1-1p36.1
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C/Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase F/111-379/Domain: protein kinase homology <KIN>
F/119-127/Region: protein kinase ATP-binding motif
F/402-468/Domain: SAM homology <SAM>

Query Match	47.7%;	Score 2476;	DB 2;	Length 478;			
Best Local Similarity	99.4%;	Pred. No. 2.7e-106;					
Matches 475;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0;			
QY	509	RARTVAGYGRYSGKMYFQMTWEAEYQTSIQEKLPLIIIGSSAAGLVFLIAVVVIAVCNRR	568				
Db	1	RARTVAGYGRYSGKMYFQMTWEAEYQTSIQEKLPLIIIGSSAAGLVFLIAVVVIAVCNRR	60				
QY	569	GPERADSEYTKLOHYTSGHMTGPKMIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIG	628				
Db	61	GPERADSEYTKLOHYTSGHMTGPKMIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIG	120				
QY	629	AGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDFLSEASIMQGFDPHPNVHLEGV	688				
Db	121	AGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDFLSEASIMQGFDPHPNVHLEGV	180				
QY	689	VTKSTPVMIIITBFMENGSLDSFLRQNDGQFTVIQLVGMRLGIAAGMKYLADNMVYVHRDLA	748				
Db	181	VTKSTPVMIIITBFMENGSLDSFLRQNDGQFTVIQLVGMRLGIAAGMKYLADNMVYVHRDLA	240				
QY	749	ARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGCKPIPIRWTAPEAIQYRKFTSASD	808				
Db	241	ARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGCKPIPIRWTAPEAIQYRKFTSASD	300				
QY	809	VMSYGIWVMEVMSYGERPYWDMTNDQVINAIEQDYRLPPPMDCPSALHQLMDCQKDRN	868				
Db	301	VMSYGIWVMEVMSYGERPYWDMTNDQVINAIEQDYRLPPPMDCPSALHQLMDCQKDRN	360				

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OM protein - protein search, using sw model

Run on: December 30, 2004, 16:41:06 ; Search time 41 Seconds
(without alignments)
1594.867 Million cell updates

Title: US-09-914-883-2
 Perfect score: 5188
 Sequence: 1 MAURRLGAALLLLPLLAAVE.....IINSIQWNRANNOIQSVEV 986

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 s

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2: /cgn2_6/pdata/1/iaa/5B_COMB pep.*
3: /cgn2_6/pdata/1/iaa/6A_COMB pep.*
4: /cgn2_6/pdata/1/iaa/6B_COMB pep.*
5: /cgn2_6/pdata/1/iaa/pTUS_COMB pep.*
6: /cgn2_6/pdata/1/iaa/backfiles1 pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query		DB	ID	Description
		Match	Length			
SUMMARIES						
1	5130	98.9	994	3	US-08-542-635-2	Sequence 2, Appli
2	5093	98.2	970	2	US-08-449-645A-11	Sequence 11, Appl
3	5093	98.2	970	2	US-08-702-367A-11	Sequence 11, Appl
4	5093	98.2	970	5	PCR-US95-04681-11	Sequence 11, Appl
5	4993.5	96.3	995	1	US-08-162-809-18	Sequence 18, Appl
6	4971.5	95.8	1011	1	US-08-162-809-12	Sequence 12, Appl
7	4962.5	95.7	995	2	US-08-673-789-5	Sequence 5, Appli
8	3929.5	75.7	984	2	US-08-673-789-6	Sequence 6, Appli
9	3723.5	71.8	951	1	US-08-162-809-2	Sequence 2, Appli
10	3669	70.7	973	1	US-08-162-809-10	Sequence 10, Appl
11	3662.5	70.6	988	1	US-08-162-809-14	Sequence 14, Appl
12	3661.5	70.6	998	2	US-08-449-645A-20	Sequence 20, Appl
13	3661.5	70.6	998	2	US-08-702-367A-20	Sequence 20, Appl
14	3661.5	69.6	970	5	PCR-US95-04681-20	Sequence 20, Appl
15	3608.5	69.6	970	2	US-08-673-789-7	Sequence 7, Appli
16	3603.5	69.5	993	1	US-08-348-143-1	Sequence 1, Appli
17	3603.5	69.5	993	1	US-08-571-785-1	Sequence 1, Appli
18	3603.5	69.5	993	3	US-09-192-435-1	Sequence 1, Appli
19	3603.5	69.5	993	4	US-09-558-340-1	Sequence 1, Appli
20	3339.5	64.4	973	1	US-08-162-809-8	Sequence 8, Appli
21	3053	58.8	991	2	US-08-449-645A-13	Sequence 13, Appl
22	3053	58.8	991	2	US-08-702-367A-13	Sequence 13, Appl
23	3053	58.8	991	5	PCR-US95-04681-13	Sequence 13, Appl
24	3049	58.8	967	2	US-08-449-645A-30	Sequence 30, Appl
25	3049	58.8	967	2	US-08-702-367A-30	Sequence 30, Appl
26	3048	58.7	953	4	US-09-751-389-7	Sequence 7, Appli
27	3046	58.7	986	2	US-08-673-789-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-542-635-2
; Sequence 2, Application US/08542635
; Patent No. 6218356
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; APPLICANT: Letwin, Kenneth
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West, Box 401
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,635
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McDiarmid, Shona S.
; REGISTRATION NUMBER: 38,798
; REFERENCE/DOCKET NUMBER: 3153-162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Embryo
; IMMEDIATE SOURCE:
; LIBRARY: lamda gt10 cDNA library
; CLONE: Combined pNURACE A2 and K2 and cDNA clones
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Distal end of chromosome 4
; MAP POSITION: near the ahd-1 mutation
US-08-542-635-2

Query Match 98.9%; Score 5130; DB 3; Length 994;

Best Local Similarity 99.5%; Pred. No. 0;
Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db	18	LLLLPLAAVEETLMDSTTATAELGVMVHPSPSGWEEVSGYDENNTIRTYQVCNVFESSQ	77
Qy	70	NNWLRTKFIARRGAHRHIVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADFDSATKTFPN	129
Db	78	NNWLRTKFIARRGAHRHIVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADFDLATKTFPN	137
Qy	130	WMENPWKVDTIAADESFSQVLDGRVWKINTEVRSFGVSRSGFYLAFOYGGCMSLIA	189
Db	138	WMENPWKVDTIAADESFSQVLDGRVWKINTEVRSFGVSRNGFYLAFOYGGCMSLIA	197

Qy	190	VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV	249
Db	198	VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV	257
Qy	250	PIGRCKAGFEAVENGTVCRGCPSTFKANQDEACTHCPINSTRTSEGATNCVCRNGY	309
Db	258	PIGRCKAGFEAVENGTVCRGCPSTFKANQDEACTHCPINSTRTSEGATNCVCRNGY	317
Qy	310	YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSDGREDLVYNNIIKSCSGSR	369
Db	318	YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSDGREDLVYNNIIKSCSGSR	377
Qy	370	GACTRCGDNVQYAPROLGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSQFASVNI	429
Db	378	GACTRCGDNVQYAPROLGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSQFASVNI	437
Qy	430	TTNQAAPSAVSIMHQVSRIVDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP	489
Db	438	TTNQAAPSAVSIMHQVSRIVDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP	497
Qy	490	TNTVTVOGLKAGAIYVQVRAVAGYGRYSGKMYFQTMTEAEVQTSIOEKLPLIGSSA	549
Db	498	TNTVTVOGLKAGAIYVQVRAVAGYGRYSGKMYFQTMTEAEVQTSIOEKLPLIGSSA	557
Qy	550	AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEAV	609
Db	558	AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEAV	617
Qy	610	REFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLS	669
Db	618	REFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLS	677
Qy	670	EASIMQFQHPNVIHLEGVVTKSTPYMIITEFMENGLSDSFLRQNDQOFTVIQVGMRLG	729
Db	678	EASIMQFQHPNVIHLEGVVTKSTPYMIITEFMENGLSDSFLRQNDQOFTVIQVGMRLG	737
Qy	730	IAAGMKYLADNMVYVHRDLAARNILVNSNLVKVYDFGLSRFLDEDDTSDPTYSALGSKIP	789
Db	738	IAAGMKYLADNMVYVHRDLAARNILVNSNLVKVYDFGLSRFLDEDDTSDPTYSALGSKIP	797
Qy	790	IRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYDMTNQDVINAIEQDYRLPPPM	849
Db	798	IRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYDMTNQDVINAIEQDYRLPPPM	857
Qy	850	DCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINPLLDRTI	909
Db	858	DCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINPLLDRTI	917
Qy	910	PDYTSFNTVDEWLEAIKMGQYKESFANAGTSDVVSQMMEDILRLGVTLAGHQKILN	969
Db	918	PDYTSFNTVDEWLEAIKMGQYKESFANAGTSDVVSQMMEDILRLGVTLAGHQKILN	977
Qy	970	SIQWRAQMNQIOSVEV 986	
Db	978	SIQWRAQMNQIOSVEV 994	

RESULT 2

US-08-449-645A-11
; Sequence 11, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA

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; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wincer, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-11

Query Match 98.2%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 15 LLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQNNWLR 74
Db 1 LLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60
Qy 75 TKFIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNWMEHP 134
Db 61 TKFIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNWMEHP 120
Qy 135 WKVYDTTAADESQVDLGGVRVSKINTEVRSFGVSRSGFYLAQDYGCGMSLIAVRVFY 194
Db 121 WKVYDTTAADESQVDLGGVRVSKINTEVRSFGVSRSGFYLAQDYGCGMSLIAVRVFY 180
Qy 195 RKPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 254
Db 181 RKPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
Qy 255 MCKAGFAVENGTVCRCPSGTFFKANQDDEACTHCPIINRTSGATNCVCRNGYYRADL 314
Db 241 MCKAGFAVENGTVCRCPSGTFFKANQDDEACTHCPIINRTSGATNCVCRNGYYRADL 300
Qy 315 DPLMPCTTTPSAQAVISSVNETSLMLETTPRDSGGREDLVNIIICKSGSGRGACTR 374
Db 301 DPLMPCTTTPSAQAVISSVNETSLMLETTPRDSGGREDLVNIIICKSGSGRGACTR 360
Qy 375 CGDNVQYAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNIITNOA 434
Db 361 CGDNVQYAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNIITNOA 420
Qy 435 APSAVSMHQSRTVDSITLSWSPDQPNQVILDEYQYKELSEYNATAIKSPNTVT 494
Db 421 APSAVSMHQSRTVDSITLSWSPDQPNQVILDEYQYKELSEYNATAIKSPNTVT 480
Qy 495 VQGLKAGAIYVQVARTVAGYGRYSGMYFQMTWTEAEYQTSIOEKLPLIIGSSAAGLV 554
Db 481 --GLKAGAIYVQVARTVAGYGRYSGMYFQMTWTEAEYQTSIOEKLPLIIGSSAAGLV 538
Qy 555 LIAVVVIAIACNRRGFERADSEYTDKLQHYTSGHMTFGMKIYIDPFYEDPNEAVREFAK 614
Db 539 LIAVVVIAIACNRRGFERADSEYTDKLQHYTSGHMTFGMKIYIDPFYEDPNEAVREFAK 598
Qy 615 EIDISCVKIEQVIGAGFGEVCSGHLKLPGRREIFVAIKTLKSGYTEKQRDFLSEASIM 674
Db 599 EIDISCVKIEQVIGAGFGEVCSGHLKLPGRREIFVAIKTLKSGYTEKQRDFLSEASIM 658
Qy 675 GQDPHPNVHLEGVVTYKTPWIIITFEMNGSLDSFLRQNDQGTFTVQLVCMRLGIAAGM 734
Db 659 GQDPHPNVHLEGVVTYKTPWIIITFEMNGSLDSFLRQNDQGTFTVQLVCMRLGIAAGM 718

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; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wincer, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-11

Query Match 98.2%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 735 KYLADMYVHRDLAARNILVSNLVCKVSDFGLSRFLFEDDTSPTTYSALGGKPIRWTA 794
Db 719 KYLADMYVHRDLAARNILVSNLVCKVSDFGLSRFLFEDDTSPTTYSALGGKPIRWTA 778
Qy 795 PEAIQYRKFTSASDVMSYGIWMHEVMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIWMHEVMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPSA 838
Qy 855 LHQLMLDCWQKDRNHRPKFCQIVNTLDKMRNPNSLKAMAPLSSGINLPLLDRTIPDYTS 914
Db 839 LHQLMLDCWQKDRNHRPKFCQIVNTLDKMRNPNSLKAMAPLSSGINLPLLDRTIPDYTS 898
Qy 915 FNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTLAGHOKKILNSIQVM 974
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTLAGHOKKILNSIQVM 958
Qy 975 RAQWNOIQSV 986
Db 959 RAQWNOIQSV 970

;
; RESULT 3
; US-08-702-367A-11
; Sequence 11, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: RPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wincer, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-11

Query Match 98.2%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 15 LLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQNNWLR 74
Db 1 LLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60
Qy 75 TKFIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNWMEHP 134
Db 61 TKFIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNWMEHP 120
Qy 135 WKVYDTTAADESQVDLGGVRVSKINTEVRSFGVSRSGFYLAQDYGCGMSLIAVRVFY 194
Db 121 WKVYDTTAADESQVDLGGVRVSKINTEVRSFGVSRSGFYLAQDYGCGMSLIAVRVFY 180
Qy 195 RKPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 254
Db 181 RKPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGR 240
Qy 255 MCKAGFAVENGTVCRCPSGTFFKANQDDEACTHCPIINRTSGATNCVCRNGYYRADL 314
Db 241 MCKAGFAVENGTVCRCPSGTFFKANQDDEACTHCPIINRTSGATNCVCRNGYYRADL 300
Qy 315 DPLMPCTTTPSAQAVISSVNETSLMLETTPRDSGGREDLVNIIICKSGSGRGACTR 374
Db 301 DPLMPCTTTPSAQAVISSVNETSLMLETTPRDSGGREDLVNIIICKSGSGRGACTR 360
Qy 375 CGDNVQYAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNIITNOA 434
Db 361 CGDNVQYAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNIITNOA 420
Qy 435 APSAVSMHQSRTVDSITLSWSPDQPNQVILDEYQYKELSEYNATAIKSPNTVT 494
Db 421 APSAVSMHQSRTVDSITLSWSPDQPNQVILDEYQYKELSEYNATAIKSPNTVT 480
Qy 495 VQGLKAGAIYVQVARTVAGYGRYSGMYFQMTWTEAEYQTSIOEKLPLIIGSSAAGLV 554
Db 481 --GLKAGAIYVQVARTVAGYGRYSGMYFQMTWTEAEYQTSIOEKLPLIIGSSAAGLV 538
Qy 555 LIAVVVIAIACNRRGFERADSEYTDKLQHYTSGHMTFGMKIYIDPFYEDPNEAVREFAK 614
Db 539 LIAVVVIAIACNRRGFERADSEYTDKLQHYTSGHMTFGMKIYIDPFYEDPNEAVREFAK 598
Qy 615 EIDISCVKIEQVIGAGFGEVCSGHLKLPGRREIFVAIKTLKSGYTEKQRDFLSEASIM 674
Db 599 EIDISCVKIEQVIGAGFGEVCSGHLKLPGRREIFVAIKTLKSGYTEKQRDFLSEASIM 658
Qy 675 GQDPHPNVHLEGVVTYKTPWIIITFEMNGSLDSFLRQNDQGTFTVQLVCMRLGIAAGM 734
Db 659 GQDPHPNVHLEGVVTYKTPWIIITFEMNGSLDSFLRQNDQGTFTVQLVCMRLGIAAGM 718
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Qy	195	RKCPRIIONGAI	FOETL	SGBAEST	SIVAARG	SCIANAE	VEVDV	PIKLYC	NGDG	EWLVP	IGRC	254																																									
Db	181	RKCPRIIONGAI	FOETL	SGBAEST	SIVAARG	SCIANAE	VEVDV	PIKLYC	NGDG	EWLVP	IGRC	240																																									
Qy	255	MCKAGFEAV	ENTV	TCRG	CPST	FRKAN	QDEA	CTH	CPIN	STT	SEGATN	CVCRNGY	RADL	314																																							
Db	241	MCKAGFEAV	ENTV	TCRG	CPST	FRKAN	QDEA	CTH	CPIN	STT	SEGATN	CVCRNGY	RADL	300																																							
Qy	315	DLPLDMPC	TTIP	SAPAR	AVISS	VNET	SLMLE	WT	PPRDS	SGRED	L	VYNI	ICK	SCSGRG	ACTR	374																																					
Db	301	DLPLDMPC	TTIP	SAPAR	AVISS	VNET	SLMLE	WT	PPRDS	SGRED	L	VYNI	ICK	SCSGRG	ACTR	360																																					
Qy	375	CGDNVQYAP	ROQL	GLTE	PR	YIIS	DL	LAHT	QYTF	EIOA	VNG	VTDS	PS	POPAS	VNIIT	TNOA	434																																				
Db	361	CGDNVQYAP	ROQL	GLTE	PR	YIIS	DL	LAHT	QYTF	EIOA	VNG	VTDS	PS	POPAS	VNIIT	TNOA	420																																				
Qy	435	APSASIMH	QVSR	T	VDS	IT	LS	WS	QD	PO	NG	VIL	YEL	QY	YKEL	SEYN	ATAIK	SPNT	VT	494																																	
Db	421	APSASIMH	QVSR	T	VDS	IT	LS	WS	QD	PO	NG	VIL	YEL	QY	YKEL	SEYN	ATAIK	SPNT	VT	480																																	
Qy	495	VOQLKAGAI	YVFO	VRAR	T	VAG	YGR	YSG	KWY	FQ	T	WEA	EY	QTS	IOE	KLP	L	LI	IGSSA	AG	LV	554																															
Db	481	--GLKAGAI	YVFO	VRAR	T	VAG	YGR	YSG	KWY	FQ	T	WEA	EY	QTS	IOE	KLP	L	LI	IGSSA	AG	LV	538																															
Qy	555	LIAVWVIA	I	VCNR	RG	ER	AD	S	EY	T	D	K	L	Q	H	Y	T	S	G	H	T	PG	M	K	I	Y	I	D	P	F	T	Y	E	D	P	N	E	A	V	R	E	F	A	K	614								
Db	539	LIAVWVIA	I	VCNR	RG	ER	AD	S	EY	T	D	K	L	Q	H	Y	T	S	G	H	T	PG	M	K	I	Y	I	D	P	F	T	Y	E	D	P	N	E	A	V	R	E	F	A	K	598								
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Db	599	EIDISCVK	IEQV	I	GAGE	F	Q	E	V	C	S	G	H	L	K	P	G	K	R	E	I	F	V	A	L	K	T	L	K	S	G	Y	T	E	K	Q	R	R	D	L	S	E	A	S	I	M	658						
Qy	675	GQFDHP	NV	I	H	E	G	V	T	K	S	P	P	V	M	I	I	T	E	F	M	E	N	G	S	L	D	S	F	L	R	Q	N	D	Q	G	T	V	I	Q	L	V	G	M	L	R	G	I	A	A	G	M	734
Db	659	GQFDHP	NV	I	H	E	G	V	T	K	S	P	P	V	M	I	I	T	E	F	M	E	N	G	S	L	D	S	F	L	R	Q	N	D	Q	G	T	V	I	Q	L	V	G	M	L	R	G	I	A	A	G	M	718
Qy	735	KYLAD	MN	V	Y	H	R	D	L	A	A	R	N	I	L	V	N	S	L	N	C	K	Y	S	D	F	G	L	S	R	F	L	E	D	D	T	S	D	P	T	S	A	L	G	K	I	P	I	R	W	T	A	794
Db	719	KYLAD	MN	V	Y	H	R	D	L	A	A	R	N	I	L	V	N	S	L	N	C	K	Y	S	D	F	G	L	S	R	F	L	E	D	D	T	S	D	P	T	S	A	L	G	K	I	P	I	R	W	T	A	778
Qy	795	PEAIQ	R	K	F	T	S	A	D	V	M	S	Y	G	I	V	M	E	V	M	S	Y	G	E	R	P	Y	D	M	T	N	Q	D	V	I	N	A	I	E	O	D	Y	L	P	P	M	C	P	S	A	854		
Db	779	PEAIQ	R	K	F	T	S	A																																													

RESULT 4

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PCT-US95-04681-11
; Sequence 11, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:

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Db 719 KYLADMYVHRDLAARNILVNSLVCKVSDFLGSRFLDDTSDPTTYSALGKGKPIIRWTA 778
Qy 795 PEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 854
Db 779 PEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 838
Qy 855 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLLDRTIPDYS 914
Db 839 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLLDRTIPDYS 898
Qy 915 FNTVDEWLEAIKMGQYKESFANAGFTSFDVVVSQMMEDILRLGVTLAGHOKKILNSIQVM 974
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSFDVVVSQMMEDILRLGVTLAGHOKKILNSIQVM 958
Qy 975 RAQNMNQISQVEV 986
Db 959 RAQNMNQISQVEV 970

RESULT 5
US-08-162-809-18
; Sequence 18, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoun G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 995 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-809-18

Query Match 96.3%; Score 4993.5; DB 1; Length 995;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

Qy 10 LLLPLLAANVEETLMDSTTATAELGWMVHPSPSGHEEYSGYDENNMNTTIRTYQVCNVFESSQ 69
Db 18 LALLPLLAANVEETLMDSTTATAELGWMVHPSPSGHEEYSGYDENNMNTTIRTYQVCNVFESSQ 77
Qy 70 NNWLRTKFIIRRGGAHRIHVMKFSVRDCSSIPSPGSKCTFNLYYYEADPDSATKTFPN 129
Db 78 NNWLRTKFIIRRGGAHRIHVMKFSVRDCSSIPNPVGSKCTFNLYYYESDFDSATKTFPN 137
Qy 130 WMENPWVKVDTIAADESFSQVDLGGVRVWKINTEVRSGFVSRSGFYLAQDYGGCMSLIA 189

Db 138 WMENPWVKVDTIAADESFSQVDLGGVRVWKINTEVRSGFVSRSGFYLAQDYGGCMSLIA 197
Qy 190 VRVYRKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL 249
Db 198 VRVYRKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL 257
Qy 250 PIGRCMKAGFEAVENGTCVRCGCPSGTFFKANQGDCACTHCPINSRTTSEGNATNCVCRNGY 309
Db 258 PIGRCMCRPGVESVENGTVCRCGCPSGTFFKASQGDGCVHCPINSRTTSEGNATNCVCRNGY 317
Qy 310 YRADLDPLDPCPTIPSAQAVISSVNETSLMELWTPPRSGGREDLVYNIICKSCSGR 369
Db 318 YRADADPVDMPCTIPSAQAVISSVNETSLMELWTPPRSGGREDLVYNIICKSCSGR 377
Qy 370 GACTRCGDNVQYAPROQLGTEPRIYISDLAHTQYTFEIOAVNGVTPQSPPOFASVNI 429
Db 378 GACTRCGDNVQYAPROQLGTEPRIYISDLAHTQYTFEIOAVNGVTPQSPPOFASVNI 437
Qy 430 TTNQAAPSAVSIMHQVSRVTDSITLSWSQDPQPNQVILDYELQYKEKSEYNATAIKSP 489
Db 438 TTNQAAPSAVSIMHQVSRVTDSITLSWSQDPQPNQVILDYELQYKEKSEYNATAIKSP 497
Qy 490 TTNVTVOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEAYQTSIOEKLPLIISSA 549
Db 498 TTNVTVOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEAYQTSIOEKLPLIISSA 557
Qy 550 AGLVFLIAVVVIAVCN-REGFERADSEYTDKLOHTYSGHMTGCMKIYIDPFTVEDPNEA 608
Db 558 AGLVFLIAVVVIAVCN-REGFERADSEYTDKLOHTYSGHMTGCMKIYIDPFTVEDPNEA 617
Qy 609 VREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 668
Db 618 VREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 677
Qy 669 SEASIMQFDPHNVHLEGVVTGSTPWNITTEPMENGLSDSFLRQNDGQFTVIQLVGMLR 728
Db 678 SEASIMQFDPHNVHLEGVVTGSTPWNITTEPMENGLSDSFLRQNDGQFTVIQLVGMLR 737
Qy 729 GIAAGMKYLADMYVHRDLAARNILVNSLVCKVSDFLGSRFLDDTSDPTTYSALGKGKI 788
Db 738 GIAAGMKYLADMYVHRDLAARNILVNSLVCKVSDFLGSRFLDDTSDPTTYSALGKGKI 797
Qy 789 PIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPP 848
Db 798 PIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPP 857
Qy 849 MDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRT 908
Db 858 MDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRT 917
Qy 909 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVVSQMMEDILRLGVTLAGHOKKIL 968
Db 918 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVVSQMMEDILRLGVTLAGHOKKIL 977
Qy 969 NSIQVMRAQNMNQISQVEV 986
Db 978 NSIQVMRAQNMNQISQVEV 995

RESULT 6
US-08-162-809-12
; Sequence 12, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoun G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego		
STATE: California		
COUNTRY: United States of America		
ZIP: 92122		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patent In Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/162,809		
FILING DATE:		
CLASSIFICATION: 514		
ATTORNEY/AGENT INFORMATION:		
NAME: Campbell, Cathryn A.		
REGISTRATION NUMBER: 31,815		
REFERENCE/DOCKET NUMBER: P-LJ 9503		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: (619) 535-9001		
TELEFAX: (619) 535-8949		
INFORMATION FOR SEQ ID NO: 12:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 1011 amino acids		
TYPE: amino acid		
TOPOLOGY: linear		
MOLECULE TYPE: protein		
US-08-162-809-12		
Query Match 95.8%; Score 4971.5; DB 1; Length 1011;		
Best Local Similarity 94.2%; Pred. No. 0;		
Matches 936; Conservative 29; Mismatches 12; Indels 17; Gaps 2;		
QY	10 LLLPLLAETLMDSTATAELGMMVHPSPGEEVGYDENNTTIRTVQCNVPSSQ	69
DB	18 LALLPLLAETLMDSTATAELGMMVHPSPGEEVGYDENNTTIRTVQCNVPSSQ	77
QY	70 NNWLRTKIRRRGAIRHIVEMKFSVRDCSSIPSPGSKETFNLYYYEADPDSATKTFPN	129
DB	78 NNWLRTKIRRRGAIRHIVEMKFSVRDCSSIPSPGSKETFNLYYYEADPDSATKTFPN	137
QY	130 WNNPWWKVDITAADESPQVDLGGVVKINTEVRSFGPVSRSGFYLAFOYGCMSLIA	189
DB	138 WNNPWWKVDITAADESPQVDLGGVVKINTEVRSFGPVSRSGFYLAFOYGCMSLIA	197
QY	190 VVVFYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL	249
DB	198 VVVFYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL	257
QY	250 PIGRCMKAGFEAVENGTVCRGCPSTGTFKANOGEACTHCPIINRTTSEGATNCVCRNGY	309
DB	258 PIGRCMKRPGYBSVENGTVCRGCPSTGTFKASQDGCVCVHCPIINRTTSEGATNCVCRNGY	317
QY	310 YRADLDPLMPCITTPSPAPQAVISSVNETSLMLEWTPPRDSGGRDLVYNIICKSCGSR	369
DB	318 YRADADPDMPCITTPSPAPQAVISSVNETSLMLEWTPPRDSGGRDLVYNIICKSCGSR	377
QY	370 GACTRCGDMVQAPRQLGLTEPRYISDILLAHTQYTFEIQAVNGVTDQSPSPQFASVNI	429
DB	378 GACTRCGDMVQAPRQLGLTEPRYISDILLAHTQYTFEIQAVNGVTDQSPSPQFASVNI	437
QY	430 TTNOAPSASVIMHQSRTVDISITLSWSQDPDNGVILDYELQYKEKSELSEYNATAIKSP	489
DB	438 TTNOAPSASVIMHQSRTVDISITLSWSQDPDNGVILDYELQYKEKSELSEYNATAIKSP	497
QY	490 TNNVTVOGLKAGAIYVQVQARTVAGYSGKMTFQWTEAEYQTSIQEKLPLIIGSSA	549
DB	498 TNNVTVOGLKAGAIYVQVQARTVAGYSGKMTFQWTEAEYQTSIQEKLPLIIGSSA	557
QY	550 AGLVFLIAVVAIVCN-RRGFERADSEYTDKLQHYTSGH-----MTPG 592	
DB	558 AGLVFLIAVVAIVCNRRRRRGERADSEYTDKLQHYTSGHSTYRGPPGGLGVRSLFVTPG 617	
QY	593 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAI 652	

Db 250 IGRCTKAGYEP-ENSVACKACAPAGTFCASOAEAGCSHCPSNSRSPSEASPICTCTRTGY 308
QY 311 RADLDPLDMPCTTTPSAQAVISSVNETSLMLETTPRDSGREDLVNLIICKSCGSGRG 370
Db 309 RADDPPEVACTSPSGRNNVISVNETSILLEWHPPRETGGRDDVTYNIICKRCADDR 368
QY 371 ACTRCGNVOYAPQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQASVNIT 430
Db 369 SCSCDDNVEVPQLGLTECRVSISSLWHTPTFDIQAINGVSSKSPFPPOHVSNIT 428
QY 431 TNOAPSASVIMHOVSRVTSITLSWQDOPNGVILDYELQYKEKELSEYNATAKSPT 490
Db 429 TNOAAPSTVPMHOVSATMSITLSWQPEOPNGIILDIYRYEKEHNEFNSMARST 488
QY 491 NTVTVOGLKAGAIYVFOVARTVAGYGRYSKMYFQTMTEAECYOTSQELPLIGSSAA 550
Db 489 NTARIDGLRPGWYVQVARTVAGYGRYSKMYFQTMTEAECYOTSQELPLIGSSAA 548
QY 551 GLVELIAVWVIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFTYEDNEAVR 610
Db 549 GVVPVSVLVAISVCSKRAYSKEAVYSDKLQHYSTGRSGPMKIYIDPFTYEDNEAVR 608
QY 611 EFAKEIDISCKIBQVTCAGFGEVGVCSGHLKLPKREIYVAIKTLKSGYTEKQRDFLSE 670
Db 609 EFAKEIDVSFKIBEVIGAGFGEVGVYKRLKLPKREIYVAIKTLKAGYSEKQRDFLSE 668
QY 671 ASIMGQDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVILVGMURGI 730
Db 669 ASIMGQDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVILVGMURGI 728
QY 731 AAGMKYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLSDTSDPTYSALGGKIP 790
Db 729 AAGMKYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLSDTSDPTYSALGGKIP 788
QY 791 RWTAPAIQVTKFTSADSVSYGIVMVEVSYGIBRPYDWMNQVINAISQDYLPPMD 850
Db 789 RWTAPAIQVTKFTSADSVSYGIVMVEVSYGIBRPYDWMNQVINAISQDYLPPMD 848
QY 851 CPSALHQLMDCWQKDRNRPKFCQIVNTLDKMRNPSLKMAMPLSSGILNPLDRTIP 910
Db 849 CPAALHQLMDCWQKDRNRPKFCQIVNTLDKMRNPSLKMAMPLSSGILNPLDRTIP 908
QY 911 DYTSTNTVDEWLEAIKMGQYKESFANAGTSTFVVSQMMEDILRLGVTLAGHOKILNS 970
Db 909 DFTAFTVDDWLSAIVMVOYRDSFLTGTSLQVLTQWTSDDLRIQVTLAGHOKILNS 968
QY 971 IQVRAQWQIQSV 984
Db 969 IHSMRVQWQNSPSV 982

RESULT 9
US-08-162-809-2
; Sequence 2, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoon G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego,
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-809-2

Query Match 71.8%; Score 3723.5; DB 1; Length 951;
Best Local Similarity 70.3%; Pred. No. 1.9e-268;
Matches 688; Conservative 121; Mismatches 117; Indels 53; Gaps 3;
QY 21 ETLMDSSTATAELGWMVHPSPSGWEEVSGYDENNTIRTYQVCNVFSSQNNWLRTKFI 80
Db 1 ETLMDSSTATAELGWMVHPSPSGWEEVSGYDENNTIRTYQVCNVFSSQNNWLRTKFI 60
QY 81 RGARHIVEMKFSVRCSSISPSVPSGCKTFNLYVEADPDSATKTFPNWMPNWKVD 140
Db 61 RGARHIVEMKFSVRCSSISPSVPSGCKTFNLYVEADPDSATKTFPNWMPNWKVD 120
QY 141 IAADESFSQVLDGRVWKNINTEVRSFGPVSRSFGYLAQDYGGCMSLIAVRVYFKCPRI 200
Db 121 IAADESFSQVLDGRVWKNINTEVRSFGPVSRSFGYLAQDYGGCMSLIAVRVYFKCPRI 147
QY 201 IQNGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKLYCNGDGEWLVPIGRMCXAGF 260
Db 148 VONFAIPPEMTGAESTSLVARTGTCTPNAEEVDVPIKLYCNGDGEWLVPIGRMCXAGF 207
QY 261 EAVENGTCVRCGSPGTFKANGQDEACTHCPINSTRITSEGTATCNCRNGYVADLDPLDMP 320
Db 208 EP-ENNVACRACFAGTFKASQAGLACRCPNRSABASPLCACRNGYVADLDPLDMP 266
QY 321 CTTIPSAQAVISSVNETSLMLETTPRDSGREDLVNLIICKSCGSGRACRGCNDVQ 380
Db 267 CTSVPSGRNVISIVNETSILLENPPRETGGRDDVTYNIICKRCADDRACRCDNVE 326
QY 381 YAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQASVNITNQAAPSAVS 440
Db 327 FVPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQASVNITNQAAPSAVS 386
QY 441 IMHOVSRVTSITLSWQDOPNGVILDYELQYKEKELSEYNATAKSPT 481
Db 387 IMHOVSRVTSITLSWQDOPNGVILDYELQYKEKELSEYNATAKSPT 446
QY 482 NATAKSPTNTVTVOGLKAGAIYVFOVARTVAGYGRYSKMYFQTMTEAECYOTSQEL 541
Db 447 NSSVARSQNTNARLEGLRPGWYVQVARTVAGYGRYSKMYFQTMTEAECYOTSQEL 506
QY 542 PLIIGSSAAGLVFLIAVWVIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFT 601
Db 507 PLIIGSSAAGLVFLIAVWVIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFT 566
QY 602 YEDPNEAVREFAKEIDISCKIBQVTCAGFGEVGVCSGHLKLPKREIYVAIKTLKAGYSE 661
Db 567 YEDPNEAVREFAKEIDISCKIBQVTCAGFGEVGVCSGHLKLPKREIYVAIKTLKAGYSE 626
QY 662 KORRDFLSEASIMGQDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVI 721
Db 627 KORRDFLSEASIMGQDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVI 686
QY 722 QLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLSDTSDPTYS 781

Db 687 QLVGMLRGIAAGMKYLAEMNYYVHRDLAARNILVNSNLVCKYDFGLSRYLQDDTSDPTT 746
Qy 782 SALGCKPIRWTAPETAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 841
Db 747 SSLGKPIRWTAPETAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 806
Qy 842 DYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 901
Db 807 DYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 866
Qy 902 LPLDRTIPDVTSTNTVDWELAKMGQYKESFANAGTSDVVSQMMEDILBLGVTLA 961
Db 867 QPLDRTIPDVTSTNTVDWELAKMGQYKESFANAGTSDVVSQMMEDILBLGVTLA 926
Qy 962 GHQKKILNSIQVRAQMNQ 980
Db 927 GHQKKILNSIQVRAQMNQ 945

RESULT 10
US-08-162-809-10
; Sequence 10, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoun G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 973 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-809-10

Query Match 70.7%; Score 3669; DB 1; Length 973;
Best Local Similarity 71.1%; Pred. No. 2.2e-264;
Matches 683; Conservative 121; Mismatches 145; Indels 12; Gaps 4;
Qy 30 TAEIGWVHPSPGHEEYSGYDENMTTQVQVNVFESSQNNWLTFTFIRRGHARHVE 89
Db 21 TSELAWTHPETGHEEYSGYDENMTTQVQVNVFESSQNNWLTFTFIRRGHARHVE 80
Qy 90 MKFSVRDCSSIPVSGCKETFNLYYEADPDSATKTFNNMNPWVKVDTIAADESFSQ 149
Db 81 LKFTVDCNSIPNIPGCKETFNLYYEADPDSATKTFNNMNPWVKVDTIAADESFSK 140
Qy 150 VDLGGRVWKINTEVRSFGPVSRSFGYLAFOQYGCMSLIAVRFYRKCPRIIQNGAIFQE 209

Db 141 LESG-----RVNTKVRSPGLSKNGFYLAFOQYGCMSLIAVRFYRKCPRIIQNGAIFQE 196
Qy 210 TLSGAESTSLVARGSCIANAEVVDVPIKLYCNGDGEWLVPICGCMCKAGFEAVENGTV 269
Db 197 TLGAEFTSLVIAAGTCIPNAVEVSVPLKLYCNGDGEWMMVPEVGACTCAAGYEPAMKOTQC 256
Qy 270 RGCPSTGTFKANQGDDEACTHCPINSRTTSEGATNCVCRNGYVRADLDPLDMECTTIPAPQ 329
Db 257 QACGPGTFKSKQGEPCSPCPNSRTTGAATVCIHSGFFRADADPADSACTSVPSAPR 316
Qy 330 AVTSVNETSLMELWTPPRDGGREDLVYNIICKSCGSGRACATCGDNTVOYARQL--- 386
Db 317 SVISVNETSLVLEWSEFPDAGGRDLDLYNVICKSCVERRLSCRDNDVEFVPRQLGLT 376
Qy 387 GLTEPRIYISDLAHTOYTFEIOAVNGVTDQSPSPQFASVNIITNQAAPSASVIMHOVS 446
Db 377 GLTERRIYISKWAHPQITFEIOAVNGISRSKPPPHFASVNIITNQAAPSASVIMHOVS 436
Qy 447 RTVDSITLSWSQDPQNGVILDYELQYKE-LSEYNATAIKSPNTVTVOGLKAGAIYV 505
Db 437 STGNSMTLSWTPPERPNIILDYELQYKEQGGQDGIANTVTSQKNSVRLDGLKANARYM 496
Qy 506 FQVRARTVAGYGRYSGMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLIIVVIAIVC 565
Db 497 VQVRARTVAGYGRYSLPTEBQTAEADGSGTSKTEQLPLIVGSATAGLLFVIVVIAIVC 556
Qy 566 NRGRFERADSEYTDKLOHTSGHMTGCMKIYIDPFTVEDPNEAREFAKEDIDISCVKIEQ 625
Db 557 FRKORNSDTPETEKQY----VTPGMKVIYIDPFTVEDPNEAREFAKEDIDISCVKIE 612
Qy 626 VIGAGEFGEVCSGHLKLPKGRKREIFVAIKLKGSGYTERKQRDFLSEASIMQFDPNVIHL 685
Db 613 VIGAGEFGEVCSGHLKLPKGRKREIFVAIKLKGSGYTERKQRDFLSEASIMQFDPNVIHL 672
Qy 686 EGVVTKSTPVIITFERMENGSLDSFLRQNDQFTVIOLVGLRGIAAGMKYLAEMNYYVHR 745
Db 673 EGVVTKSRPVIITFERMENCALDSFLRQNDQFTVIOLVGLRGIAAGMKYLAEMNYYVHR 732
Qy 746 DLAAARNILVNSNLVCKYDFGLSRYLQDDTSDPTTSAIGGKPIRWTAPETAIQYRKFTS 805
Db 733 DLAAARNILVNSNLVCKYDFGLSRYLQDDTSDPTTSAIGGKPIRWTAPETAIQYRKFTS 792
Qy 806 ASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQYRPLPPMDCPSALHQLMDCQK 865
Db 793 ASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQYRPLPPMDCPSALHQLMDCQK 852
Qy 866 DRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGINLPLDRTIPDVTSTNTVDWELAI 925
Db 853 DRNLRPKFGQIVNTLDKMRNPNLSKAMAPLSSGINLPLDRTIPDVTSTNTVDWELAI 912
Qy 926 KMGQYKESFANAGTSDVVSQMMEDILBLGVTLGHHOKKILNSIQVRAQMNQIOSVE 985
Db 913 KMGYKESFANAGTSDVVSQMMEDILBLGVTLGHHOKKILNSIQVRAQMNQIOSVE 972
Qy 986 V 986
Db 973 V 973

RESULT 11
US-08-162-809-14
; Sequence 14, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoun G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700

```

; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-809-14

Query Match 70.6%; Score 3662.5; DB 1; Length 998;
Best Local Similarity 70.1%; Pred. No. 6.9e-264;
Matches 684; Conservative 121; Mismatches 144; Indels 27; Gaps 5;

QY 30 TAEIGWVHPSPGVEEYGVYDENNTIRTVQCVNPFSSQNNMLRTKFIIRRGGAHRHVE 89
DB 21 TSELATWTHETGVEEYGVYDENNTIRTVQCVNPFSSQNNMLRTKFIIRRGGAHRHVE 80
QY 90 MKFSVRDCSSIPSPGCKETFNLYEADPDSATKTFPNMNMENPWYKVDITIAADEFSQ 149
DB 81 LKFTVRDCNSIPNPGCKETFNLYEADPDSATKTFPNMNMENPWYKVDITIAADEFSK 140
QY 150 VDLGGRVKNINTEVRSGPVSRSFYLAFOYDGCMSLIAVRVYRKCPRILQNGAIFQE 209
DB 141 LESG---RVNTRKVSFGLSKNGFYLAFOYDGCMSLIAVRVYRKCPRILQNGAIFPE 196
QY 210 TLSGAESTSLVAARGSCIANAEVDVPLKLYCNGDGEWLVPIGRMCCKAGFEAVENGTV 269
DB 197 TLTGAEFTSLVIACTCLPNAVFVSPLKLYCNGDGEWLVPIGRMCCKAGFEAVENGTV 256
QY 270 RGCPSGTIFKANQGDCACTHCPINSRTTSEGATNCVCRNGYRADLPLDMPTTIPSAQ 329
DB 257 QACGPGTIFKSKQGGPCSPCPNRTTAGAATVTCICRSGPRADADPADGACTSVPSAPR 316
QY 330 AVISSVNETSLMLWTTPRDSGGREDLVNLIICKSCSGRCACTRCGDNVQYAPROL--- 386
DB 317 SVISSVNETSLMLWTTPRDSGGREDLVNLIICKSCSGRCACTRCGDNVQYAPROL--- 376
QY 387 GLTEPRYISDLAHTOYTFEIQAVNGVTDSPSPQFASVNTTNOAAPSVAIVHQS 446
DB 377 GLTERRIYISKMAHPQTFEIQAVNGVTDSPSPQFASVNTTNOAAPSVAIVHQS 436
QY 447 RTVDSITLSWSQPPQNGVILDYELQYKE-LSEYNATAIKSPNTVTVOGLKAGAIYV 505
DB 437 STGNSMTLSWTPPRNGIILDYBIKSEKQCGQDGIANTVTSQKNSVRLDGLKANARYM 496
QY 506 FOVPARTVAGRYSGRMVFTMTAEVQTSIQEKLPLIIGSSAAGVFLIAVVIAIVC 565
DB 497 VQVARTVAGRYSGRMVFTMTAEVQTSIQEKLPLIIGSSAAGVFLIAVVIAIVC 556
QY 566 NRRGF-----BRADSEYTDKQLHYTSGHMTGPMKIYIDPFTYEDNEAVR 610
DB 557 FRKGMVTEQLSSPLGRKQRNSTDPEYTEKLQY-----VTPGMKIYIDPFTYEDNEAVR 612
QY 611 EFAKEIDISCVKIEEYVIGAGEFGEVGRGLKLPGRREIFVAIKTLKVGTERQRRDRLSE 670

613 EFAKEIDISCVKIEEYVIGAGEFGEVGRGLKLPGRREIFVAIKTLKVGTERQRRDRLSE 672
671 ASIMGQFDHPNVTHLEGVVTKSTPVMIIITEFWENGSLDGLRNDGQFTVIOLVGMLRGI 730
673 ASIMGQFDHPNVTHLEGVVTKSTPVMIIITEFWENGSLDGLRNDGQFTVIOLVGMLRGI 732
731 AAGMKYLAADNVYVHRDLAARNILVNSNLVCKYSDFGLSRFLFLEDDTSDPTTYSALGKPI 790
733 AAGMKYLAADNVYVHRDLAARNILVNSNLVCKYSDFGLSRFLFLEDDTSDPTTYSALGKPI 792
791 RMTAPEAIQYRKFTSASDVMSYGIWVMSYGERPYWDMTNOVINAEQDYRLPPMD 850
793 RMTAPEAIQYRKFTSASDVMSYGIWVMSYGERPYWDMTNOVINAEQDYRLPPMD 852
851 CPSSALHQLMDCWQDRNHRPKGQIVNTLDKWRPNLSIKAMAPLSSGILPLDRTIP 910
853 CPTALHQLMDCWQDRNHRPKGQIVNTLDKWRPNLSIKAMAPLSSGILPLDRTIP 912
911 DYTSEMTVDWLEAIKMGYKESFANAGFTSFDVVSQMMEDILRLGVTLIAGHQKILNS 970
913 DYTFTTVDWLEAIKMGYKESFANAGFTSFDVVSQMMEDILRLGVTLIAGHQKILNS 972
971 IQVRAQMNOIOSVEV 986
973 IQVRAQMNOIOSVEV 988

RESULT 12
US-08-449-645A-20
; Sequence 20, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-20

Query Match 70.6%; Score 3661.5; DB 2; Length 998;
Best Local Similarity 70.2%; Pred. No. 8.3e-264;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

QY 10 LLLIPLI-----AAVEETLMDSTTAEALGWMVHPSPGVEEYGVYDENNTIRTVQVCN 63
DB 23 LLLIPLI-----AAVEETLMDSTTAEALGWMVHPSPGVEEYGVYDENNTIRTVQVCN 62
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Qy 64 VFSSQNNWLRTKPIRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYEADPDSA 123
Db 83 VRESSQNNWLRTGFIWRDQVRVVELKFTVRDCNSIPNIPGSKCTFNLYYEADSDVA 142
Qy 124 TKTFPNNMNPWKVDITIAADESFQVLDLGRVWKNINTEVRSFGPVSRSFYLAFOYGG 183
Db 143 SASPFNNMNPYKVDITIADESFRLDAG----RVNTKVRSFGPLSKAGFYLAFOQGA 198
Qy 184 CMSLIAVRVYRKCPIIQAAGTGAETLSAAGSCLVAAGSCIANAEVDVPIKLYCNG 243
Db 199 CMSLISVRAFYKCASTAGTALPPELTGAETSLVIAAGTCLIPNAVEVSPKLKLYCNG 258
Qy 244 DGEWLVPIGRMCCKAGFEAVENGTCVRCGSPGTGFKANQGDCACTHCPINSRTTSEGATNC 303
Db 259 DGEWLVPIGRMCCKAGFEAVENGTCVRCGSPGTGFKANQGDCACTHCPINSRTTSEGATNC 318
Qy 304 VCRNGYTRADLPLDMPCCTTIPSAQAVISSVNETSLMELWTPPRDGGEDLVYNIICK 363
Db 319 TCHNFFRADSDSADACTVPSPPRGVSNVNETSLILEWSEPRDLGVDRDLDLYNVICK 378
Qy 364 SC--GSGRGACTRCGNVQVAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFS 421
Db 379 KCHGAGASACSCDDNVFVPRQLGSEPRVHTSHLLAHTRYTFEIQAVNGVSGK3PLP 438
Qy 422 PQFASVNTTNAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDEYQYKELSEY 481
Db 439 PRYAANVNTTNAAPSEVPTRLRLHSSGSSLTLSWAPPERNGVILDEYKMEK--SEG 496
Qy 482 NATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSKMYFQWTWE--ABYQTSLOEK 540
Db 497 IASTVTSQMSVQLDGLRPDARYVQVARTVAGYGRYSKMYFQWTWE--ABYQTSLOEK 556
Qy 541 LPLIIGSSAAGLVFLAVVIAIIVCLRKQRHSGDSEYTEKLOQY----IAPGMKYIDPF 600
Db 557 LPLIVGSATAGLVFVAVVIAIIVCLRKQRHSGDSEYTEKLOQY----IAPGMKYIDPF 612
Qy 601 TYEDPNEAVREFAKEIDI SCVKIEQVIGAGEFGEVCSGHLKLPGRKIFVIAITKLSGYT 660
Db 613 TYEDPNEAVREFAKEIDVSCVKEIEVIGAGEFGEVCSGHLKLPGRKIFVIAITKLSGYT 672
Qy 720 EKORRDFLSASINGQFDHPNVIHLEGVVTKSTPVMILITFEMENGSLDSEFLRNDGQFTV 720
Db 673 ERQRDFLSASINGQFDHPNVIHLEGVVTKSTPVMILITFEMENGSLDSEFLRNDGQFTV 732
Qy 721 IQLVGLRGTAAGKYLADNMYVHRLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 780
Db 733 IQLVGLRGTAAGKYLSEMYVHRLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 792
Qy 781 TSALGGKIPIRWTAPEAIQVRKFTSASDVNSYGIWMEVNSYGERPYWDMTNQDVINAIE 840
Db 793 TSSLGKIPIRWTAPEAIQVRKFTSASDVNSYGIWMEVNSYGERPYWDMTNQDVINAIE 852
Qy 841 QDYRLPPMPCPSALHQLMDCWQDRNHRPKQIYVNTLDKMRNPNLSKAMAPLSSGI 900
Db 853 QDYRLPPMPCPSALHQLMDCWQDRNHRPKQIYVNTLDKMRNPNLSKAMAPLSSGI 912
Qy 901 NLPLDRTIPDYTSFNTVDEWLEAKIMQVYKESFANAGTSTFSDVWSOMMEDILRLGVTL 960
Db 913 SQPLDRTIPDYTSFNTVDEWLEAKIMQVYKESFANAGTSTFSDVWSOMMEDILRLGVTL 972
Qy 961 AGHOKILNSIQVNRQAQNMQIQSV 986
Db 973 AGHOKILNSIQVNRQAQNMQIQSV 998

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RESULT 13

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US-08-702-367A-20
; Sequence 20, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine
; Kinases

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; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-20

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Query Match 70.6%; Score 3661.5; DB 2; Length 998;
Best Local Similarity 70.2%; Pred. No. 8.3e-264;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

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Qy 10 LLLLPL-----AAVEETLMDSTTAAELGMMVHPSPSGEESGYDENMNTIRTYQVCN 63
Db 23 LLLLPLLLPAGCALAETLMDTKWTSELAWTSHPSGEEVSGYDENMNTIRTYQVCN 82
Qy 64 VFSSQNNWLRTKPIRRGAHRIHVEMKFSVRDCSSIPSPGSKCTFNLYYEADPDSA 123
Db 83 VRESSQNNWLRTGFIWRDQVRVVELKFTVRDCNSIPNIPGSKCTFNLYYEADSDVA 142
Qy 124 TKTFPNNMNPWKVDITIAADESFQVLDLGRVWKNINTEVRSFGPVSRSFYLAFOYGG 183
Db 143 SASPFNNMNPYKVDITIADESFRLDAG----RVNTKVRSFGPLSKAGFYLAFOQGA 198
Qy 184 CMSLIAVRVYRKCPIIQAAGTGAETLSAAGSCLVAAGSCIANAEVDVPIKLYCNG 243
Db 199 CMSLISVRAFYKCASTAGTALPPELTGAETSLVIAAGTCLIPNAVEVSPKLKLYCNG 258
Qy 244 DGEWLVPIGRMCCKAGFEAVENGTCVRCGSPGTGFKANQGDCACTHCPINSRTTSEGATNC 303
Db 259 DGEWLVPIGRMCCKAGFEAVENGTCVRCGSPGTGFKANQGDCACTHCPINSRTTSEGATNC 318
Qy 304 VCRNGYTRADLPLDMPCCTTIPSAQAVISSVNETSLMELWTPPRDGGEDLVYNIICK 363
Db 319 TCHNFFRADSDSADACTVPSPPRGVSNVNETSLILEWSEPRDLGVDRDLDLYNVICK 378
Qy 364 SC--GSGRGACTRCGNVQVAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFS 421
Db 379 KCHGAGASACSCDDNVFVPRQLGSEPRVHTSHLLAHTRYTFEIQAVNGVSGK3PLP 438
Qy 422 PQFASVNTTNAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDEYQYKELSEY 481
Db 439 PRYAANVNTTNAAPSEVPTRLRLHSSGSSLTLSWAPPERNGVILDEYKMEK--SEG 496
Qy 482 NATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSKMYFQWTWE--ABYQTSLOEK 540
Db 497 IASTVTSQMSVQLDGLRPDARYVQVARTVAGYGRYSKMYFQWTWE--ABYQTSLOEK 556
Qy 541 LPLIIGSSAAGLVFLAVVIAIIVCLRKQRHSGDSEYTEKLOQY----IAPGMKYIDPF 600
Db 557 LPLIVGSATAGLVFVAVVIAIIVCLRKQRHSGDSEYTEKLOQY----IAPGMKYIDPF 612

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QY 601 TYEDPNEAVREFAKEIDISCVKLEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYT 660
DB 613 TYEDPNEAVREFAKEIDVSCVKEEVIGAGEFGEVCRGLKQPGREVEVAIKTLKSGYT 672
QY 661 EKQRDPLSEASIMGQFDHPNVIHLGCVTKSTPPVMIITEFMENGLSDSFLRQNDGQFTV 720
DB 673 ERQRDPLSEASIMGQFDHPNVIHLGCVTKSTPPVMIITEFMENGLSDSFLRQNDGQFTV 732
QY 721 IQLVGMRLGTAAGKYLADNMYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 780
DB 733 IQLVGMRLGTAAGKYLSEWYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 792
QY 781 TSALGGKIPIRWTAPEAIOYRKFTSASDVMSYGIWVMSYGERPYWDMTNDQVINAIE 840
DB 793 TSSLGKIPIRWTAPEAIOYRKFTSASDVMSYGIWVMSYGERPYWDMNQDVINAIE 852
QY 841 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900
DB 853 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 912
QY 901 NLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVTL 960
DB 913 SQPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVTL 972
QY 961 AGHOKKILNSIQVWRAQMNQIOSVEV 986
DB 973 AGHOKKILNSIQVWRAQMNQIOSVEV 998

RESULT 14

PC-TUS95-04681-20
; Sequence 20, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Patent Operations/RW
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PC-TUS95-04681-20

Query Match 70.6%; Score 3661.5; DB 5; Length 998;
Best Local Similarity 70.2%; Pred. No. 8.3e-264;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;
QY 10 LALLPLLL-----AAVEETLMDSTTATAGLGMVHPGSGWEEVSGYDENMNTIRTYQVCN 63
DB 23 LLLPLLLPAGRALEETLMDTKWTSSELATWSHESGWEEVSGYDEAMNPIRTYQVCN 82

QY 64 VFESSQNNWLTKEFIRRRGAHRHIVEMKFSVRDCSSIPSVPSCKETFNLYYYEADPDSA 123
DB 83 VRESSQNNWLTKEFIRRRGAHRHIVEMKFSVRDCSSIPSVPSCKETFNLYYYEADPDSA 142
QY 124 TKTEPNMNMENPWKVDITAADESFQVDLGRVVMKINTEVRSGPVSRSFYLAFOYGG 183
DB 143 SASPFWMENFYVVDITAADESFQVDLGRVVMKINTEVRSGPVSRSFYLAFOYGG 198
QY 184 CMSLIAVVRFKCPRIIONCAIFOETLSGAESTSLVAARGSCIANAEEDVDVPIKLYCNG 243
DB 199 CMSLISVRAFYKCASTTAGFALFPETITGAETPSLVIAPGTCLPNAVEVSVPLKLYCNG 258
QY 244 DGMVLPIRCWCCKAGFEAVENGTVCRGCPSTGFKAMQDEACTHCPINSTRITSEGTATC 303
DB 259 DGMVWVPGACTCATGHEPAKESQCRPCPPGSKAKQGEPCPCPPNSRTTSPAASIC 318
QY 304 VCRNGYYPADLDLPMPCTTIPSAPOAVISSVNETSLMELTTPRDSGREDLVNICK 363
DB 319 TCHNNFYRADSDSADACTTVPSPRGVISNNETSLILEWSEPRDLGVRDDLNVNICK 378
QY 364 SC--GSGRGACTRCGDNVQYAPROGLTEPRYISDLAHTQYTFEIQAVNGVTDQSPFS 421
DB 379 KCHGAGSASACRCDNVFVPRQLGLSEPRVHTSHLLAHTRYTFEVQAVNGVSGKSLP 438
QY 422 PQFASVNIITNOAPSASVIMHQVSRVTSITLSWSQDPQNGVILDYELQYKELSEY 481
DB 439 PRYAAVNIITNOAPSEVPTLRLHSSGSLTSLWPPERPNGVILDYEMKIFYE--SEG 496
QY 482 NATAKSPNTVTVOGLKAGAIYVQVARTVAGVGRYGRMYFQMTYE-AEYQTSIOEK 540
DB 497 IASTVTSQNNVQLDGLRDPDARYVQVARTVAGVGRYGRMYFQMTYE-AEYQTSIOEK 556
QY 541 LPLIGSSAAGLVFLIAVAVVIAIVCNRRGRFERADSEYTDKLOHYTSGHMTQMKIYIDPF 600
DB 557 LPLIGSSAAGLVFLIAVAVVIAIVCNRRGRFERADSEYTDKLOHYTSGHMTQMKIYIDPF 612
QY 601 TYEDPNEAVREFAKEIDISCVKLEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYT 660
DB 613 TYEDPNEAVREFAKEIDISCVKLEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYT 672
QY 661 EKQRDPLSEASIMGQFDHPNVIHLGCVTKSTPPVMIITEFMENGLSDSFLRQNDGQFTV 720
DB 673 ERQRDPLSEASIMGQFDHPNVIHLGCVTKSTPPVMIITEFMENGLSDSFLRQNDGQFTV 732
QY 721 IQLVGMRLGTAAGKYLADNMYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 780
DB 733 IQLVGMRLGTAAGKYLSEWYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 792
QY 781 TSALGGKIPIRWTAPEAIOYRKFTSASDVMSYGIWVMSYGERPYWDMTNDQVINAIE 840
DB 793 TSSLGKIPIRWTAPEAIOYRKFTSASDVMSYGIWVMSYGERPYWDMNQDVINAIE 852
QY 841 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900
DB 853 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 912
QY 901 NLPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVTL 960
DB 913 SQPLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVTL 972
QY 961 AGHOKKILNSIQVWRAQMNQIOSVEV 986
DB 973 AGHOKKILNSIQVWRAQMNQIOSVEV 998

RESULT 15

US-08-673-789-7
; Sequence 7, Application US/08673789
; Patent No. 5614479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 970
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-7

Query Match 69.6%; Score 3608.5; DB 2; Length 970;
Best Local Similarity 70.1%; Pred. No. 7e-260;
Matches 672; Conservative 116; Mismatches 161; Indels 9; Gaps 3;

Qy 30 TAEIGMWHPPSGWEEVSGYDENNTIRTYQCVNVPFSSQNNMLRTKFIIRRGAIHIVE 89
Db 21 TSELATHTTETGWEVSGYDEAMQPIRTYQCVREAAQQOQMLRTKFINQDVQRYVE 80
Qy 90 MKFSVRDCSSIPSPVSGCKETFNLYYIYADPDSATKTFPNMNMENPWVKVDTIADESFSQ 149
Db 81 LKFTVRDCKSIPKIPGSKETFNLYYIYADPDSATKTFPNMNMENPWVKVDTIADESFSK 140
Qy 150 VDLGGRVKNKTEVRSFGVSRSGFYLAFOYDGCMSLIARVVFYRKCPIRQNGALFOE 209
Db 141 LESG-----RVNTRKVSFGPSKNGFYLAFOYDGCMSLIARVVFYRKCPIRQNGALFOE 196
Qy 210 TLGSAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMCKGAEVAVENGTVG 269
Db 197 TLGAEPTSLVIAFGTCIPQAVEVSVPKLYCNGDGEWLVPIGRCMCKGAEVAVENGTVG 256
Qy 270 RGCPSGTFFKANGQDEATHCPINRSTTSSEGNATNCVCRNGYYRADLPLDMPCTTIPAPQ 329
Db 257 QACGPGTFFKANGQDEATHCPINRSTTSSEGNATNCVCRNGYYRADLPLDMPCTTIPAPQ 316
Qy 330 AVTSSVNETSLMLETTPRDSGGEDLVNIIKSCSGRGACTRCGDNVQYAPROGLT 389
Db 317 SVISVNETSFVLEWSPQAGGRDILLXNVICKCSVERRLCSRDDNVEFVRQGLT 376
Qy 390 EPRYISDLAHTOYTFEIOAVNGVTDQSPSPFASVNTTNOAAPSVAVSIMHOVSRTV 449
Db 377 ERYISVWNAHPQYTFEIOAVNGVTDQSPSPFASVNTTNOAAPSVAVSIMHOVSRTV 436
Qy 450 DSITLSWSQPPQPPNGVILDVLOYEKE-LSEYNATAIKSPTNTVTVOGLKAGAIYVQV 508

Db 437 NSMTLSWTPPERENGILDEYIKYSEKQGGDGIANTVTTSQKNSVRDLGLKANARYMVQV 496
Qy 509 RARTVAGYGRYSGMYFQWTAEAYOTSIOEKLPLIIGSSAAGLVFLIAVVVIAIVCNRR 568
Db 497 RARTVAGYGRYSLPTEFQTAEADGTSKTEQELPLIVGSATAGLLFVVVVIAIVCFRK 556
Qy 569 GPERADSEYTDKLOHYTSGHMTFGMKIYIDPFTYEDPNEAVREFAKESIDISCVKIEVIG 628
Db 557 QRNSTDPEYTEKLQY-----VTPGMKVYIDPFTYEDPNEAVREFAKESIDISCVKIEVIG 612
Qy 629 AGSEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDRDFLSEASIMGQFDPHNVHLEGV 688
Db 613 AGSEFGEVCRGLKPGKREIFVAIKTLKVGTYTERQRDRDFLSEASIMGQFDPHNVHLEGV 672
Qy 689 VTGSTPVMIIITEPMENGSLSDFLRQNDGQFTVTLQVGLMGLGIAAGMKYLDAMNYYVHRDLA 748
Db 673 VTGSRPVMIVTEEMENCALDSFLRLNDGQFTVTLQVGLMGLGIAAGMKYLDAMNYYVHRDLA 732
Qy 749 ARNVLNSNLVKVSDPGLSRFLEDDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASD 808
Db 733 ARNVLNSNLVKVSDPGLSRFLEDDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASD 792
Qy 809 VMSYGIWMEVMSYGERPYWDMTNOVINAIEODYRLPPMDCEALHQLMDCWQKDRN 868
Db 793 VMSYGIWMEVMSYGERPYWDMTNOVINAIEODYRLPPMDCEALHQLMDCWQKDRN 852
Qy 869 HRPKFGQIVNTLDKMIWNPNSLKAMAPLSSGINLPLDRTIPDYSPTNTVDWELEAKMG 928
Db 853 LRPKFAQIVNTLDKLIENNAASLVIAVSGVSGVQPLADRVDPYTFITTVGDMLDALKMG 912
Qy 929 QYKESFANAGFTSFDVVSQMMEDILRLGVTLGAGHKILNSIQVMRAQNNQIQSV 986
Db 913 RYKENFVNHGFSFSLVAQWTAEDLLRIGVTLGAGHKILNSIQVMRAQNNQIQSV 970

RESULT 16

US-08-348-143-1
Sequence 1, Application US/08348143
GENERAL INFORMATION:
APPLICANT: TAJIMA, HISAO
APPLICANT: KITAGAWA, KOICHIRO
APPLICANT: OHNO, HIROYUKI
APPLICANT: UENO, TOSHIO
TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs
TITLE OF INVENTION: encoding it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,143
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 993 amino acids	
TYPE: amino acid	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
ORIGINAL SOURCE:	
ORGANISM: rat	
TISSUE TYPE: skeletal muscle myoblast	
CELL LINE: L6	
US-08-348-143-1	
Query Match 69.5%; Score 3603.5; DB 1; Length 993;	
Best Local Similarity 68.5%; Pred. No. 1.7e-259;	
Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;	
QY	17 AAVETLMDSTATA-----ELGVMVHPSPGWEVSGYDENNTIRTY 59
Db	11 AAARAAAEATNSILVRPTSEGRIDSEFVELAWTSHPESGWEVSAYDEAMNPIRTY 70
QY	60 QVCNVFSSQNNWLRTKFIIRRGGAHRHVEMKFSVRDCSSIPSPGSKCTENLYYYEAD 119
Db	71 QVCNVRESSQNNWLRTGFIWRREVQRYVVELKFTVRDCNSIPNIPGSKCTENLYYYEAD 130
QY	120 FDSATKTFPPNMENPVKVDITIAADESFQVDLGGVRVMKINTEVRSFGPVSRSGFYLAFO 179
Db	131 SDVASASSPFWMENPVKVDITIADESFRLDAG---RVNKTVRSFGPLSKAGFYLAFO 186
QY	180 DYGCMSLIAVRVYKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANABEVDVPIKL 239
Db	187 DQGCMSLISVRAFYKCKASTAGTALFPETLTGAETPSLVIAPGTCTIANAVEVSVELKL 246
QY	240 YCNGDGEWLPIGCMCKAGFEAVENGTVCRGCGSGTGFKANQGDCACTHCPINRSTTSEG 299
Db	247 YCNGDGEWMVPGACTCATGHEPAKETQCACPGSKAKQGGCPCLPCPPNRSRTSPA 306
QY	300 ATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDIVYN 359
Db	307 ASICTCHNNFYRADSDTADSACTVPSPRGVINSVNETSLILEWSEPRDILGGRDDLLYN 366
QY	360 IICKSCSGRGA-----CTRCGDNVQAPROGLTEPRIVYISDLLAHTOYTFEIQAVNGV 414
Db	367 VICRKGSSGAGGATCSCRDDNVFEPQLGTERKRVHSHLLAHTRYTFEIQAVNGV 426
QY	415 TDQSPSPQFASVNITTTQAAPSASVIMHVSRTVDSITLSWSQPDOPNGVILDELYQYY 474
Db	427 SGKSLPFRYAANVTINQAAPSEVPTLHLHSSGSSLTLSWAPPERENGVLIDYEMKYP 486
QY	475 EKELSEYNATAIKSTNTVTVOGLKAGAIYVQVRAARTVAGYGRYSGMYTQWTE-AEY 533
Db	487 EK--SKGIATVTSQKNSVQLDGLQPDARYVQVRAARTVAGYGYQYRPAEFETTSERGS 544
QY	534 QTSIQEKLPLIIGSSAAGLVFLIAVVTAIVCNRGPERADSEYTDKLOHYTSGHMTPGM 593
Db	545 AQQLQEQLEPLIVGSTVAGVFVMMVVVVVIALVCLRKQRGQPDAREYTEKLQYY----VAPRM 600
QY	594 KIYIDPFYEDNEAVRFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRRIFFVAIK 653
Db	601 KYVIDPFYEDNEAVRFAKEIDVSCVKEIEVIGAGEFGEVCRGLKLPGRREVFVAIK 660
QY	654 TLKSYTKQRDFLSEASIMQFDPHNVHLEGVVTKSTPVMILTEFMEVNGSLDSFLRQ 713
Db	661 TLKVGYTERQRDFLSEASIMQFDPHNIIRLEGVVTKSRFVMILTEFMEVNCALDSFLRL 720
QY	714 NDGQFTVLQVLMGLGIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVSDFGLSRPLED 773
Db	721 NDGQFTVLQVLMGLGIAAGMKYLSMMYFVHRDLAARNILVNSNLVCKVSDFGLSRFLED 780
QY	774 DTSPTYTSALGCKPIRWTAPAIQYRKFTSASDVWSYIGIVMVEVMSYGERPYWDMTNQ 833
Db	781 DFDSDPTYTSLSLGGKPIRWTAPAIQYRKFTSASDVWSYIGIVMVEVMSYGERPYWDMNSQ 840
QY	834 DVINAIEQDYRLPPMDCCSALHOLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAM 893
Db	841 DVINAVEQDYRLPPMDCCPAALHQLMLDCWVRDRNLRPKFSQIVNTLDKLRNAAASKVI 900

Db 131 SDVASASPPFMENPYVVDIADPDESFRDLADG-----RVNKKVRSFGPLSKAGFYLAQ 186
Qy 180 DYGGCMSLIAVRVYRKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVVDVPIKL 239
Db 187 DOGACMSLISVRAFYKCASTAGTAGFALPPELTGAEPTSLVIAPTCIANAWEVSVPKL 246
Qy 240 YCNGDGEWLVPIGRMCKAGFEAVENGTVCRGCGSGTFFKANQDEACTHCPINRSTTSEG 299
Db 247 YCNGDGEWLVPIGRMCKAGFEAVENGTVCRGCGSGTFFKANQDEACTHCPINRSTTSPA 306
Qy 300 ATNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLETWTPRDSGGREDLVYN 359
Db 307 ASICTCHNNFYRADSDTADACTTVPSPRGVIVSNVNETSLILEWSEPRDLGGDDLLYN 366
Qy 360 IICKSCSGRGA-----CTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGV 414
Db 367 VICCKRSGSGAGGATPCSCDDNVEPEPRQLGLTERRVHSHLLAHTRYTFEIQAVNGV 426
Qy 415 TDQSPFPQFASVNTTNOAAPSIVSMQVSRVDSITLSWSQDOPNGVILDYELQYY 474
Db 427 SGKSPLPRYAAVNTTNOAAPSIVPTLHSHSSGSSLTLSWAPPRNGVILDYEMKYF 486
Qy 475 EKEISEYNATAIKGPTNTVTVQGLKAGAIYVFOYRARTVAGYGRYSGWYFQWTE-ABY 533
Db 487 EK--SKGIASVTTSOKNSVQDGLQDPARYVYVQVARTVAGYGRYSPAEFTTSRSGS 544
Qy 534 QTSIQEKLPLIIGSSAGLVFLIAVWIAIVCNRRGFERADSEYTDKLQHYTSHGMTPGM 593
Db 545 AQLQEQPLIVGSTVAGFVWVWVIALVCLRKQRPDAEYTEKLOQY----VAPRM 600
Qy 594 KIYIDPFTYEDPNBAVREFAKEIDI SCVKIEQVITGAGEFGEVCSGHLKLPGRKIFVIAIK 653
Db 601 KVIYIDPFTYEDPNBAVREFAKEIDVSCVKBIEVIGAGEFGEVCRGLKLPGRREVFVIAIK 660
Qy 654 TLKSGYTEKORRDFLSEASIMQDHPNVHLEGVTKSTPVMIIITFEMENGLSDSLRQ 713
Db 661 TLKVGTYERQRDRDFLSEASIMQDHPNIIRLEGVTKSRVPMIITBFMENCALDLSFRL 720
Qy 714 NDGQFTVQLVGLMGLGIAAGKYLADNMVYHRDLAARNILVNSLVCKVSDPGLSRFLED 773
Db 721 NDGQFTVQLVGLMGLGIAAGKYLSEMMYVHRDLAARNILVNSLVCKVSDPGLSRFLED 780
Qy 774 DTSPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIIVMVEVMSYGERPVDWMTNQ 833
Db 781 DPSDPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIIVMVEVMSYGERPVDWMTNQ 840
Qy 834 DVINAISQDYVLPDPMDCPSALHQLMDCWOKDRNHPKFCQIYVNTLDMKIRNPNLSKAM 893
Db 841 DVINAISQDYVLPDPMDCPSALHQLMDCWDRNLRPKFSQIYVNTLDMKIRNPNLSKAM 900
Qy 894 APLSSGINLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVSVSOMMEDI 953
Db 901 ASAPSGMSQPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVSVSOMMEDI 960
Qy 954 LRLGVTLAGHOKTILNSIQVNRQMNQISQVEV 986
Db 961 LRLGVTLAGHOKTILNSIQVNRQMNQISQVEV 993

RESULT 18
US-09-192-435-1
; Sequence 1, Application US/09192435
; Patent No. 6303320
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09192,435
APPLICATION NUMBER: US/09192,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,785
FILING DATE: 13-DEC-1995
APPLICATION NUMBER: 08/348,143
FILING DATE: 23-NOV-1994
APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: skeletal muscle myoblast
CELL LINE: L6
US-09-192-435-1

Query Match 69.5%; Score 3603.5; DB 3; Length 993;
Best Local Similarity 68.5%; Pred. No. 1.7e-259;
Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;
Qy 17 AAVEETLMDSTTATA-----ELGMVHPSPGWEVSGVDENMTTIRTY 59
Db 11 AAAAEEAATNSLSILVRPTSEGRISDFEVELAMTSHPEGSWEVSAVDAMNPIRTY 70
Qy 60 QVCNVPESSNNMLRTKFIERRGAHRITHVEMKFSVRDCSSIPVPSGCKETENLYYYEAD 119
Db 71 QVCNVRESSNNMLRTGFIWRREVQVYVELKFTVRDCNSIPNIPGCKETFNLFYYEAD 130
Qy 120 FDSATKTFPMWMPVVKVDITIAADESFQVDLGGVRVMKINTEVRSFSPVSRSGFYLAQ 179
Db 131 SDVASASPPFMENPYVVDIADPDESFRDLADG-----RVNKKVRSFGPLSKAGFYLAQ 186
Qy 180 DYGGCMSLIAVRVYRKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVVDVPIKL 239
Db 187 DOGACMSLISVRAFYKCASTAGTAGFALPPELTGAEPTSLVIAPTCIANAWEVSVPKL 246
Qy 240 YCNGDGEWLVPIGRMCKAGFEAVENGTVCRGCGSGTFFKANQDEACTHCPINRSTTSEG 299
Db 247 YCNGDGEWLVPIGRMCKAGFEAVENGTVCRGCGSGTFFKANQDEACTHCPINRSTTSPA 306
Qy 300 ATNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLETWTPRDSGGREDLVYN 359
Db 307 ASICTCHNNFYRADSDTADACTTVPSPRGVIVSNVNETSLILEWSEPRDLGGDDLLYN 366
Qy 360 IICKSCSGRGA-----CTRCGDNVQYAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGV 414
Db 367 VICCKRSGSGAGGATPCSCDDNVEPEPRQLGLTERRVHSHLLAHTRYTFEIQAVNGV 426
Qy 415 TDQSPFPQFASVNTTNOAAPSIVSMQVSRVDSITLSWSQDOPNGVILDYELQYY 474
Db 427 SGKSPLPRYAAVNTTNOAAPSIVPTLHSHSSGSSLTLSWAPPRNGVILDYEMKYF 486

QY 774 DTSPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQ 833
DB 781 DPSPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQ 840
QY 834 DVINAIBODVRLPPMPCPSALHMLDCKQKDRNHRPKGQIVNTLDKMRNPSLKAM 893
DB 841 DVINAVSQDRLLPPMPCPSALHMLDCKQKDRNHRPKGQIVNTLDKMRNPSLKAM 900
QY 894 APLSSGILNLLDRTIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDI 953
DB 901 ASAPSGMSQPLLDRTIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDI 960
QY 954 LRIGVTLAGHOKKILNSIQVRAQMQIQSVVEV 986
DB 961 LRIGVTLAGHOKKILNSIQVRAQMQIQSVVEV 993

RESULT 20

US-08-162-809-8
; Sequence 8, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pascuale, Elena B.
; APPLICANT: Sajjadi, Pereyoun G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 973 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-809-8

Query Match 64.4%; Score 3339.5; DB 1; Length 973;
Best Local Similarity 63.1%; Pred. No. 7.5e-240;
Matches 615; Conservative 150; Mismatches 197; Indels 13; Gaps 6;
QY 21 ETLMDSTATAELGCMVHPSPGMEVSGYDENMMNTIRTYQVNCVFSSQNNWLRTKFIIR 80
DB 3 ELLDTTGETSEIGWTSHPPDGMEVSRDDEKQIITFQVNCNMFQNNWLRTKFIIR 62
QY 81 RGAHRHVEKMFVRDCSSIPSPVSGCKETFNLYYEADEFDSATKTPFNWNPWVKVD 140
DB 63 RGAHRVHRLHFSVRDCASMRVASTCKETFTLYHQSDVDIASQELPEWHEGFWTKVD 122
QY 141 IAADESESOVDLGRVNMKINTEVRSFGVRSRGLAFQDYGGCMSLIARVFRKCPRI 200
DB 123 IAADESESOVDLGRVNMKINTEVRSFGVRSRGLAFQDYGGCMSLIARVFRKCPAV 182

QY 201 IQNGALFOETLSGAESTSLVAARGSCIANAEEDVDP-----IKLYCNGDGEMLVPIGRMC 256
DB 183 VKGFASFPETTFAGGERTSLVESLGTGVANAEASTTSSGSGVRLHCNCEGEMVATGRCS 242
QY 257 KAGFEAVENGTCTGCGSPSTFKANQGDREACTHCPIINSRT--TSEGATNCVCRNGYYRADL 314
DB 243 KAGYQSDNENQACQACPIGSKASVGDGDCCLCPAHSHAPLPLFGFSECTECQCSQSHYAS 302
QY 315 DPLDMPTCTTIPSAQVAISSVNETSLMLETTPRDSGREDLVNIIKCKSGS--GRGACT 373
DB 303 DNSDAPCTGTPSAPRDLSEIYVGSNVLLTWRLPKDLGGRKDVFNVLCKECPRSATCTV 362
QY 374 RCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTQSPSPQFASVNIITNQ 433
DB 363 RCGDNVQFEPQVGLTESRVQVSNLLARVQYTFEIQAVNLVLTLSSEAPQYATINVTSTQ 422
QY 434 AAPSAVSIHVOVSRVDSITLSWSQDPDNGVILDYELQYVEKELSELYNATAIKSPNTV 493
DB 423 SVPSAIPMMHQSRSATSSITLSWPPQDPQNGVILDYELQYVEKELSELYNATAIKSPNTV 482
QY 494 TVOGLKAGAIYVQVRAARTVAGYGRYSGKMYFOTMTAEAYQTSIQEKLPLIISSAGLV 553
DB 483 TIINLSPGKIYVQVRAARTVAGYGRYSGKMYFOTMTAEAYQTSIQEKLPLIISSAGLV 542
QY 554 FLI--AVVIAIYVNRGRGERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAVRE 611
DB 543 FLVIAIAILAIIFKSK--RRETPVTRDQYVISTRGL--GVKYIDPSTYEDPNEAIRE 598
QY 612 FAKEDISCVKIEQVIGAGEFGEVCSGHLKPKGREIFVAKITLKSQYTKQRDFLSEA 671
DB 599 FAKEDIVSFKIEBEVIGSGEFCFGRKHPGKREYTVAKITLKSQYTKQRDFLSEA 658
QY 672 SIMQFDPHNVHLEGVVTKSTPVMITPEMENGSLDSFLRQNDGQFTVQLVGLRGIA 731
DB 659 SIMQFDPHNVHLEGVVTKSTPVMITPEMENGSLDSFLRQNDGQFTVQLVGLRGIA 718
QY 732 AGMKYLADMYVHRDLAARNILVNSNLVCKVSPDGLSRFLEDDTSDPTYSALGGKIPR 791
DB 719 AGMKYLSDMYVHRDLAARNILVNSNLVCKVSPDGLSRFLEDDTSDPTYSALGGKIPR 778
QY 792 WTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQVINAIDQYRLPPPPDC 851
DB 779 WTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQVINAIDQYRLPPPPDC 838
QY 852 PSALHMLDCKQKDRNHRPKGQIVNTLDKMRNPSLKAMAPLSSGILNLLDRTIPD 911
DB 839 PTVLHLLMLDCKQKDRNHRPKGQIVNTLDKMRNPSLKAMAPLSSGILNLLDRTIPD 898
QY 912 YTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDIILRLGVTLAGHOKKILNSI 971
DB 899 FPSLSNAHEWLDKMGYKESFANAGFTSFVVSQMMEDIILRLGVTLAGHOKKILNSI 958
QY 972 QVRAQMQIQSVVEV 986
DB 959 QLMKVLHNLQLEPVEV 973

RESULT 21

US-08-449-645A-13
; Sequence 13, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA

725 GMLRGIAAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSAL 784
 733 GMLRGISAGMKYLSMDMGVYHRDLAARNILVNSLVCKVDFGLSRVLEDD-PEAAVTR- 790
 785 GKKIPIRWTAPETAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAISQDYR 844
 791 GKKIPIRWTAPETAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAISQDYR 850
 845 LPPMDCPFSALHOLMDCWOKDRHPRKFGQIVNTLDDKMRNPNLSLKAMAPLSSGINLPL 904
 851 LPSMDCFAALYQLMDCWOKERNRPRKFDIENMLDKLRNFSSSLKTLVNSCRVSNLL 910
 905 LDRTIPDVTSENTVDWLEAKMQYKESFANAGFTSFVVSQMMEDILRLGVTLAQHG 964
 911 AHSPLGSGAYRSVGEWLEAKMGRYTEIFWENGYSSMDAVAQVTLSDRLRLGLVTLVGHQ 970
 965 KKLNSIQVMRAQM 978
 971 KKLNSIQVMRAQM 984

RESULT 22
 US-08-702-367A-13
 ; Sequence 13, Application US/08702367A
 ; Patent No. 5981246
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Gary M.
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
 ; TITLE OF INVENTION: Kinases
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Amgen Patent Operations/RW
 ; STREET: 1840 Behavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/702,367A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-287
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 991 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-702-367A-13

Query Match 58.8%; Score 3053; DB 2; Length 991;
 Best Local Similarity 58.8%; Pred. No. 1.6e-218; Indels 12; Gaps 9;
 Matches 573; Conservative 165; Mismatches 224;
 QY 6 LGALLLLPLAAVEETLMDSTTATLGLMVMHPPSGWEVSGYDENMTIRYQVCNVF 65
 DB 22 LCAALRTLLASPSNEVLLDSRTVMGLDWIAFPKNGWEEIGVDENYAPIHTYQVCVM 81
 QY 66 ESSQNNWLRTKPIRRGAHRIHVMKESVDCSSISVPSGCKETNLNLYYEAADFDSATK 125
 DB 82 EQNNQNLTLTWSINEGASRIFELKFTLRDCNSLPGGLGTCKETFMWYFESDDQNGR- 140
 QY 126 TFPNMENPWKVDITIAADESFQVLDLGRVMKINTEVRSFGVSRSGFYLAFOYGGCM 185
 DB 141 ---NIKENQYIKIDTIAADESFTELDDLRVMKLNTEVROVGLPKKGFYLAFOYGGACI 197

ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,645A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-287
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 991 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-449-645A-13

Query Match 58.8%; Score 3053; DB 2; Length 991;
 Best Local Similarity 58.8%; Pred. No. 1.6e-218; Indels 12; Gaps 9;
 Matches 573; Conservative 165; Mismatches 224;
 QY 6 LGALLLLPLAAVEETLMDSTTATLGLMVMHPPSGWEVSGYDENMTIRYQVCNVF 65
 DB 22 LCAALRTLLASPSNEVLLDSRTVMGLDWIAFPKNGWEEIGVDENYAPIHTYQVCVM 81
 QY 66 ESSQNNWLRTKPIRRGAHRIHVMKESVDCSSISVPSGCKETNLNLYYEAADFDSATK 125
 DB 82 EQNNQNLTLTWSINEGASRIFELKFTLRDCNSLPGGLGTCKETFMWYFESDDQNGR- 140
 QY 126 TFPNMENPWKVDITIAADESFQVLDLGRVMKINTEVRSFGVSRSGFYLAFOYGGCM 185
 DB 141 ---NIKENQYIKIDTIAADESFTELDDLRVMKLNTEVROVGLPKKGFYLAFOYGGACI 197
 186 SLIAVRFVRKPRIIQNGAIFOETLSGAESTSLVAARGSLCIANAEEVDVPIKLYCNGDG 245
 198 ALVSRVYKCPVSRVHLAVPDFTITGADSQLLEVSGCV-NHSVTDPEPKMHCASRG 256
 246 EMLVPIGRCMKAGFEAVNGVTCRCGSPGTFKANGQDEACTHCPINSRTTSEGATNCVC 305
 257 EMLVPIGRCMKAGFEAVNGVTCRCGSPGTFKANGQDEACTHCPINSRTTSEGATNCVC 314
 306 RNYGYPADLDPLDMPCTTIPSPAPQAVISVNETSLMLETTPRDSGGREDLVNMLCKSC 365
 315 EKDYFRRESDPPTMACTRPSPAPRNASVNETSVFLEWIPPADTGGGRKDVSYIACKKC 374
 366 GSRGACTRCGDNVQAPRLGLTEPRIYISDLAHTQVTEPIQAVNGVTQSPSPQFA 425
 375 NSHAGVCECGHVRVLPQSGKLNKTSVMVLLAHTNFTFIEAVNGVSDLSFGARQYV 434
 426 SVNITNQAPSAVSIMHVSRTVDSITLSWSQOPNGVILDYELQYKELSYNATA 485
 435 SVNITNQAPSPVTVNKKGIKAGISLSWQBPDRPNGLIILEYIKHFKED-QETSITI 493
 486 IKSPNTVTVQGLKAGAIYVQVARTVAGYSGKMYFOTMTEAEYOTSIOEKLPLII 545
 494 IKSKETTITAEGLKPAVYVQIRATAGYVFSRFEFET-TPVFAASSQSQIPVIA 552
 546 GSSAAGLVFLIAVVAIVCNRRGFERADSEYTDKLQHYTGHM-TPGMKVIIDPFTYED 604
 553 VSVTVGVILLAVVIGVLLSGRRGYSKAKQDPEERKMFMHNGHILKPGVTVTIDPHTYED 612
 605 PNEAVREFAKEIDISCVKIIOVIGAGEFVCSGHLKLPCKREIFVAIKTLKSGVTEKOR 664
 613 PNQAVHEFAKEIEASCITIERVIGAGEFVCSGRLKLPCKRELPAIKTLKSGVTEKOR 672
 665 RDLFSEASIMQFDPHNVHLEGVVTKSTPMIITEFMENGLSDLSLRQNDQOFTVIQLV 724
 673 RDLFSEASIMQFDPHNVHLEGVVTKSTPMIITEFMENGLSDLSLRQNDQOFTVIQLV 732

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Qy 186 SLIARVYFKCPRIQNGAIFQETLSGARSTSLVAARGSCIANAEVDVPIKLYCNGDG 245
Db 198 ALVSRYVYKCPBVRHLAVFPDITGADSSQLLEVSVCV-NHSTVDPEPKMHCABG 256
Qy 246 EWLVPICRCCKAGFAEAVENGTCRCGPGSTFKANQDEACTHCPINSRTTSEGATNCVC 305
Db 257 EWLVPICRCCKAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPPHSYTHEEASTSCVC 314
Qy 306 RNGYRADLPLDMPCTTIPSAQVAIVSSNETSLMLEWTPPRDSGGREDLVNIIKSC 365
Db 315 EKDYFRRESPPPTMACTRPPSAPRNAISNVNETSVFLEWIPPADTGGKDVSVYIACKKC 374
Qy 366 GSGRGACTRCGDNVQVAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFA 425
Db 375 NSHAGVCECGHVRYPLOSGLKNTSVMMVDLLAHTNYTFEIAVNGVSDLSFGARQYV 434
Qy 426 SVNITNOAAPSIVSMHVSRTVDSITLSWSOPDQNGVILDVLEQYKEKSEYNATA 485
Db 435 SVNITNOAAPSIVNVKGIKANSISLSWQEPDRNGIILEYIHKFKD-QETSYTI 493
Qy 486 IKSPNTNTVVOGLKAGAIYVQVRAITVAGYGRYSGRMVYFQMTAEAYQTSIOEKLPLII 545
Db 494 IKSKETITAEGLKPAASVYVQIRARTAGYGVFSRFEFET-TPVFAASDQSQIPVIA 552
Qy 546 GSSAAGLVFLIAVVIAVNCNRGFRERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYED 604
Db 553 VSVTVGVILLAVVIGVLLSGRRCGYSKAKODPEEKMHFNHGHIKLPGVRTYIDPHTYED 612
Qy 605 PNEAVREFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTKSGYTEKOR 664
Db 613 PNOAVHEFAKEIEASCITIERVIGAGEFEGVCSGRLKLPGRRELPLVAIKTKVGYTEKOR 672
Qy 665 RDLSEASIMGQFDHPNVHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQLV 724
Db 673 RDLFGEASIMGQFDHPNI IHLEGVVTKSPMIIVTEYMWENGSLDTFLKKNQGQFTVIQLV 732
Qy 725 GMLRGIAAGKYLADNMVYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPTYSAL 784
Db 733 GMLRGISAGKYLSDMGVYHRDLAARNILVNSNLVCKVDFGLSRVLEDD-PEAAVYTR- 790
Qy 785 GGIPIRWTAPATQYRKFTSASDVWSYGVIMVMSYGERPYWDMTNQDVINAIEQDYR 844
Db 791 GGIPIRWTAPATAFRKFTSASDVWSYGVIMVMSYGERPYWDMTNQDVINAIEQDYR 850
Qy 845 LPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPL 904
Db 851 LPPPMDCPSALYQLMLDCWQKERNRPKFDIENVMDKLIERNPSSLKLTVNASCRVSNLL 910
Qy 905 LDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDIILRLGVTLAGHQ 964
Db 911 AEHSPLSGAYSRSVGEWLEAIKMGRYTEIFPMENGYSSMDAVAQVTLDELRLRLGVTLVGHQ 970
Qy 965 KKIINSTOVMAOM 978
Db 971 KKIINSTOVMAOM 984
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RESULT 23

PCT-US95-04681-13

; Sequence 13, Application PC/TUS9504681

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; NUMBER OF INVENTION: Kinases

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Angen Patent Operations/RBW

; STREET: 1840 Dehaviiland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04681-13
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Query Match 58.8%; Score 3053; DB 5; Length 991;
Best Local Similarity 58.8%; Pred. No. 1.6e-218;
Matches 573; Conservative 165; Mismatches 224; Indels 12; Gaps 9;

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Qy 6 LGAALLLLPLLAVEETLMDSTTATAEGLMVMVPPSGWEVSGYDENMNTIRTYQVNCVP 65
Db 22 LCAALRTLASPSNEVNLLDSRTVMGDLGWIAPFKNGWEEIGEDENYAPIHTYQVCKVM 81
Qy 66 ESSONWLRTKFIARRGAHRIHVEMKFSVRDCSSIPSVCCKETFLNLYTYEADFDSATK 125
Db 82 EQONNWLTSISNEGASRIFELKFLTRDCNSLPGGLGTCKETFNMYIFESDDQNGR- 140
Qy 126 TFPNMENPMVKYDITAADESFSQVDLGRVMKINTEVRSFGVRSRSGFYLAFOYDGC 185
Db 141 ---NIKENQYIKIDITAADESFTELDLDGRVMKLNTEVRDVGPLSKKGFYLAFOVGACI 197
Qy 186 SLIARVYFKCPRIQNGAIFQETLSGARSTSLVAARGSCIANAEVDVPIKLYCNGDG 245
Db 198 ALVSRYVYKCPBVRHLAVFPDITGADSSQLLEVSVCV-NHSTVDPEPKMHCABG 256
Qy 246 EWLVPICRCCKAGFAEAVENGTCRCGPGSTFKANQDEACTHCPINSRTTSEGATNCVC 305
Db 257 EWLVPICRCCKAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPPHSYTHEEASTSCVC 314
Qy 306 RNGYRADLPLDMPCTTIPSAQVAIVSSNETSLMLEWTPPRDSGGREDLVNIIKSC 365
Db 315 EKDYFRRESPPPTMACTRPPSAPRNAISNVNETSVFLEWIPPADTGGKDVSVYIACKKC 374
Qy 366 GSGRGACTRCGDNVQVAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFA 425
Db 375 NSHAGVCECGHVRYPLOSGLKNTSVMMVDLLAHTNYTFEIAVNGVSDLSFGARQYV 434
Qy 426 SVNITNOAAPSIVSMHVSRTVDSITLSWSOPDQNGVILDVLEQYKEKSEYNATA 485
Db 435 SVNITNOAAPSIVNVKGIKANSISLSWQEPDRNGIILEYIHKFKD-QETSYTI 493
Qy 486 IKSPNTNTVVOGLKAGAIYVQVRAITVAGYGRYSGRMVYFQMTAEAYQTSIOEKLPLII 545
Db 494 IKSKETITAEGLKPAASVYVQIRARTAGYGVFSRFEFET-TPVFAASDQSQIPVIA 552
Qy 546 GSSAAGLVFLIAVVIAVNCNRGFRERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYED 604
Db 553 VSVTVGVILLAVVIGVLLSGRRCGYSKAKODPEEKMHFNHGHIKLPGVRTYIDPHTYED 612
Qy 605 PNEAVREFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTKSGYTEKOR 664
Db 613 PNOAVHEFAKEIEASCITIERVIGAGEFEGVCSGRLKLPGRRELPLVAIKTKVGYTEKOR 672
Qy 665 RDLSEASIMGQFDHPNVHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQLV 724
Db 673 RDLFGEASIMGQFDHPNI IHLEGVVTKSPMIIVTEYMWENGSLDTFLKKNQGQFTVIQLV 732
Qy 725 GMLRGIAAGKYLADNMVYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPTYSAL 784
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733 GMLRGISAGMKYLDGMYVHRDLAARNILNSLVCKVDFGLSRVLEDD-PEAAVYTR- 790
785 GGIPIRWTAPALQVARKFTSASDVMSYGVVMVEVMSYGERPYWDMTNOQVINAIBQDYR 844
791 GGIPIRWTAPALQVARKFTSASDVMSYGVVMVEVMSYGERPYWDMTNOQVINAIBQDYR 850
845 LPPMDPCSAHQMLDCWQKORNRHPPKQIIVNTLDKMRNPNLSKAMAPLSSGINLPL 904
851 LPPMDPCSAHQMLDCWQKORNRHPPKQIIVNTLDKMRNPNLSKAMAPLSSGINLPL 910
905 LDRIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLVGHQ 964
911 AHSPLGSGAYRSVGEWLEAKMGRYTEIFWNGYSMDAVAQVTLDELRLGVTLVGHQ 970
965 KKIILNSIQVMRAQM 978
971 KKIILNSIQVMRAQM 984

RESULT 24.
US-08-449-645A-30
Sequence 30, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-645A-30

Query Match 58.8%; Score 3049; DB 2; Length 967;
Best Local Similarity 59.0%; Pred. No. 3.1e-218;
Matches 572; Conservative 165; Mismatches 219; Indels 14; Gaps 10;

12 LPLLAALV--EETLMDSTTATAEALGMVHPSPGWEVSGYDENMNTHTYQVNVFESSQ 69
2 LRTLLASPSNEVNLDSRTVMDGLWIAFPKNGWEEIGEDVENDAPIHTYQVCKVMEQNG 61
70 NNWLRTKFTRRGAHRIHVEMKFSVDCSSIPSVGSKCTFNLYVEADPDSATKTPN 129
62 NNWLLTSWISNAGSRIFELKFTLRDCNSLPGGLGTCKFTFNMYPFSSDQNGR---N 117
130 WNNPWNKVTDTAADESFSQVLDGGRVKNINTEVASFVGRSGFYLAQDYGGMCLIA 189
118 IKENQVIKIDTAADESFTLDDGDRVKNLNTEDVDGVLKKGFLAFQDVGCIALVS 177
190 VRFVYKCPRIITONGAIFQETLGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL 249

178 VVVYKCKPSVVRHLAVFPDITGADSSQLLEVSSCV-NHVSVDPEPPMKCSAEGEWLV 236
250 FIGRCMKAGFEAVENGTVCGCPSTGTPKANOGDACHCTCPINRTTSEGATNCVCRNGY 309
237 FIGRCMKAGFEAVENGTVCGCPSTGTPKANOGDACHCTCPINRTTSEGATNCVCRNGY 294
310 YRADIPLDMPCTTTPSAPOAVISSVNETSLMELWTPRDSGGREDLVYNIICKSCSGSR 369
295 FRRESDPPTMACTRPSPAPRNAISNVNETSVFLEWIPADTGGKDVYIYACKCNSHA 354
370 GACTRCGDNVQYAPRQLGLTEPRIYISDLAHTQVTFEIQAVNGVTDOSPSPQASVNI 429
355 GVCBEGGHVYLRQSGGLKNTSVMMVLLAHTNYTFEIEAVNGVSDLSPGARQVSVNV 414
430 TTNQAAPSAVSMHVOVSRVDSITLSWQDPDQPNVILDYELQVYVEKELSEYNATAIKSP 489
415 TTNQAAPSPVTNVKKGIAKNSISLSWQEPDQPNVILDYELQVYVEKELSEYNATAIKSP 473
490 TMTVTVOGLKAGAIYVFOVARTVAGYRGYSKMYFOTMTEAEYQTSIQEKLPLIIGSSA 549
474 ETTITAEGLKPAVSVVFIQIRARTAGYGVFSRPFET-TPVFAASSDQSQIPVIAVSVT 532
550 AGLVFLIAVVIIVCNRRGFERADSEYTDKLQHTSGHM-TPGMKIYIDPETYEDPNEA 608
533 VGVILLAVVIGVLLSGRCGYSKAKQDPEEKXMHFNHGHKILPGVRTYIDPHTYEDPNEA 592
609 VREFAKEIDISCVKLEOVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDL 668
593 VHEFAKEIEASCITIERVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDL 652
669 SEASIMQGFDPNVIHLEGVVTSTPMIITBEMNGSLDSFLRQNDGQFTVQLVGMRL 728
653 GEASIMQGFDPNVIHLEGVVTSTPMIITBEMNGSLDSFLRQNDGQFTVQLVGMRL 712
729 GIAAGKYLADMYVHRDLAARNILNSLVCKVDFGLSRLEDDTPTVTSALGGKI 788
713 GISAGMKYLDGMYVHRDLAARNILNSLVCKVDFGLSRLEDD-PEAAVYTR-GGKI 770
789 PIRWTAPALQVARKFTSASDVMSYGVVMVEVMSYGERPYWDMTNOQVINAIBQDYR 848
771 PIRWTAPALQVARKFTSASDVMSYGVVMVEVMSYGERPYWDMTNOQVINAIBQDYR 830
849 MDCPSALHQLMLDCWQKORNRHPPKQIIVNTLDKMRNPNLSKAMAPLSSGINLPLDRT 908
831 MDCPSALHQLMLDCWQKORNRHPPKQIIVNTLDKMRNPNLSKAMAPLSSGINLPLDRT 890
909 IPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLVGHQKIL 968
891 PLGSGAYRSVGEWLEAKMGRYTEIFWNGYSMDAVAQVTLDELRLGVTLVGHQKIL 950
969 NSIQVMRAQM 978
951 NSIQVMRAQM 960

RESULT 25
US-08-702-367A-30
Sequence 30, Application US/08702367A
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-30

Query Match 58.8%; Score 3049; DB 2; Length 967;
Best Local Similarity 59.0%; Pred. No. 3.1e-218;
Matches 572; Conservative 165; Mismatches 219; Indels 14; Gaps 10;
12 LLPLLAIV--EETLMDSTTATAGLWVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ 69
2 LRTLLASPSNEVLLDSRTVMGLWIAFPKNGWEEIGEVDENYAPHTTYQVCKVMEQNG 61
70 NNWLRTFERRGAHRHIVEMKFSVRDSSIPSPGCKETFNLYYEADPDSATKTFPN 129
62 NNWLLTSWISNEGASRIFELKFTLRDCNSLPGGLGTCKTFNNYFESDDQNGR----N 117
130 WMENPVKVDITIAAESFSDVLDGRVWVHPPSGVSRSGFYLAPODYGCMSLIA 189
118 IKENQYIKIDTIAADESFTLDDGRVWVHPPSGVSRSGFYLAPODYGCMSLIA 177
190 VRVYRKPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLV 249
178 VRVYKCPVWRLHAFVPPDITGADSSQLLEVSQV-NHSTVDPPKMHCSAEGEWLV 236
250 PIGRCMKAGFEAVENGTVCRGCPSTFKANQDEACTHCPINSTRTSSEAGATNCVCRNGY 309
237 PIGRCMKAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDY 294
310 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSSGGREDLVNIIKSCSGSR 369
295 FRRESDPPTWACTPPSAPRNAISNVNETSVFLEWIPADTGGKDVSYIACKNCNSHA 354
370 GACTRCGDNVQYAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNI 429
355 GVCBECGHRVYLPQSGLKNTSVMMVYDLLAHTNYTFEIEAVNGVSDLSFGARQYVSVNV 414
430 TTNOAAPSANVIMHOVSRTVDSITLSQSDQPNQNGVLDLYEYKELSEYNATAIKSP 489
415 TTNOAAPSNTVKKGIKNSISLSQEPDRPNGIILEYKHFEXD-QETSYTIKSK 473
490 TINTVVOGLKAGALYVFOVARTVAGYRGYSGMYFOTMTEAEYQTSIQEKLPLIGSSA 549
474 ETTITAGLKPASVYVQIARTAAAGYGVSRREFET-TPVFASSDDQIQIPVIAVSVT 532
550 AGLVFLIAVVVIAIVCNRRGFERADSEYTKLQHYTSGHM-TPGMKIYIDPFTYEDPNEA 608
533 VGVLLAVVGLLSGRRGCVSKAQDPPEEKMHFNHGIKLPGRVYIDPHTYEDPNQA 592
609 VREPAKIDISCVKIEQVIGAGEGVCCHLKLPGKREIFVAIKTLKSGYTEKQRDPL 668
593 VHEPAKIEASCITIERVIGAGEGVCCHLKLPGKRELVAIKTLKVGYTEKQRDPL 652
669 SEASIMGOFDHPNVIHLEGVVTKTTPVMIITERMENGSLDSFLRNDQGFVIOGVMLR 728
653 GEASIMGOFDHPNVIHLEGVVTKSKPMVITVEMENGSLDFTFLKNDQGFVIOGVMLR 712
729 GIAAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLBDDTSDPTTYSALGGKI 788

Db 713 GISAGMKYLSDMGYVHRDLAARNILVNSLVCKVSDFGLSRVLDD-PEAAYTTR-GGKI 770
Qy 789 PIWTAPEALQYKFTSASDVMSYGVIMVWVMSYGERPYWDMTNQDVINAIEQDYRLPPP 848
Db 771 PIWTAPEALAFKFTSASDVMSYGVIMVWVMSYGERPYWDMTNQDVINKAVEGYRLPSP 830
Qy 849 MDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGILPLLDRT 908
Db 831 MDCPAALYQLMLDCWQKERNRPFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAHS 890
Qy 909 IPDYSFNTVDEWLEBAIKQYKESFANAGFTSFVVSQMMEDILRLGVTLAGHQKIL 968
Db 891 PLGSGAYRSVGEWLEAIKGRYTEIFMENGYSMDAVAQVTLDELRLRLGVTLAGHQKIM 950
Qy 969 NSIQVMRAQM 978
Db 951 NSIQEMKVL 960
RESULT 26
US-09-751-389-7
; Sequence 7, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Human
US-09-751-389-7

Query Match 58.8%; Score 3048; DB 4; Length 953;
Best Local Similarity 59.2%; Pred. No. 3.6e-218;
Matches 568; Conservative 164; Mismatches 216; Indels 12; Gaps 9;
Qy 20 EETLMDSTTATAGLWVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQNWLRTKFR 79
Db 3 EVNLLDSRTVMGLWIAFPKNGWEEIGEVDENYAPHTTYQVCKVMEQNNWLLTSWIS 62
Qy 80 RRGARHIVEMKFSVRDSSIPSPGCKETFNLYYEADPDSATKTFPNNMENPWVKVD 139
Db 63 NEGASRIFELKFTLRDCNSLPGGLGTCKTFNNYFESDDQNGR----NIKENQYIKID 118
Qy 140 TIAADESFSDVLDGRVWVHPPSGVSRSGFYLAPODYGCMSLIAVRVYRKP 199
Db 119 TIAADESFTELDGRVWVHPPSGVSRSGFYLAPODYGCMSLIAVRVYRKP 178
Qy 200 IIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLVPIGRCKMCKAG 259
Db 179 VVRHLAVPPTIIGADSSQLLEVSQV-NHSTVDPPKMHCSAEGEWLVPIGRCKMCKAG 237
Qy 260 FEAVENGTVCRGCPSTFKANQDEACTHCPINSTRTSSEAGATNCVCRNGYRADLDPLDM 319
Db 238 YEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDYFRRESDDPTM 295
Qy 320 PCTTIISAPQAVISSVNETSLMLEWTPPRDSSGGREDLVNIIKSCSGSGACTRCGDNV 379
Db 296 ACTRPPSAPRNAISNVNETSVFLEWIPADTGGKDVSYIACKNCNSHAGVCEBCEGHHV 355
Qy 380 QYAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNOAAPS 439
Db 356 RYLPRGGLKNTSVMMVYDLLAHTNYTFEIEAVNGVSDLSFGARQYVSVNTTNOAAPS 415
Qy 440 SIMHOVSRTVDSITLSQSDQPNQNGVLDLYEYKELSEYNATAIKSPNTVTVOGLK 499

[illegible]

		NAME: Winter, Robert B.	
		REFERENCE/DOCKET NUMBER: A-287	
		INFORMATION FOR SEQ ID NO: 15:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 986 amino acids	
		TYPE: amino acid	
		TOPOLOGY: linear	
		MOLECULE TYPE: protein	
		US-08-702-367A-15	
		Query Match	58.7%; Score 3045; DB 2; Length 986;
		Best Local Similarity	59.3%; Pred. No. 6.4e-218;
		Matches	580; Conservative 146; Mismatches 212; Indels 40; Gaps 12;
Qy	18	AVEETLMDSTTATAELGWMVHP-PSGWEVSGYDENMNTIRTYQVCNVFSSQNNWLRTK	76
Db	28	ANEVTLLDSRSVQELGWIASPLEGGWEVSIIMDEKNTPIRTYQVCNVMEPSQNNWLRTD	87
Qy	77	FIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSDATKTFPNWMENPVW	136
Db	88	WITREGARVVEIKFTLRDCNSLPFGYMGCKETFNLYYESDNDKERFI-----RENQFV	143
Qy	137	KVDITAADESFOVDLGRVNMKINTEVRSPGSKETFNLYYEADFDSDATKTFPNWMENPVW	196
Db	144	KIDITAADESFTQVDIGDRIMKLNTEIRDVGPLSKGFLAFQDVGACIALVSRVFYK	203
Qy	197	CPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGELWPIGRMC	256
Db	204	CPLTVRNLAQPPDITGADTSSLVEVRGSCVNNSEEDVP-KMYCGADGELWPIGNCLC	262
Qy	257	KAGFEAVENGIVCRGCPSGTFFKANQDEACTHCPINSRTTSEGATNCVCRNGYYRADLDP	316
Db	263	NAGHE--ERSGEQACKIGYKALSTDTATCAKCPHYSVWEGATSCDGRGFRADNDA	320
Qy	317	LDMPCTTIPSAQAVISSVNETSLMLETWTPRDSGGREDLVNIIKSCSG-RCGATRC	375
Db	321	ASMPCTPPSAPLNLISNNVNETSNLEWSSPQNTGGRQDISYNNVCKKCGAGDPKCRPC	380
Qy	376	GNVOYAPROGLTEPRIYISDLAHTQYTEIOAVNGVTDQSPSPQFASVNTNQAA	435
Db	381	GSQVHTPQNGLTKTKVTSITDLAHTNYTEIWAIVNGSVKYNPNPQSVSVTTNQAA	440
Qy	436	PSAVISMQHVSRTVDSITLSQSDQDPNGVILDYELQYKELSEYNATAIKSPNTNTVV	495
Db	441	PSSIALVQAEKTRYSVALAWLEDPDPNGVILEYEVKYEDQKQERSVIRVTAARNDI	500
Qy	496	QCLKAGAIYVQVARTVAGYCRVSGKMYFQMTAEAYQTSIQEKLK-LIIGS-----	547
Db	501	KGLNELTSYVPHVARTAAAGYDFSEPLEVTNT-----VPSRIIGDGANSTVL	549
Qy	548	--SAAGLVFLAVVIAVCHRR--GPERADSEYTDKLOHTSGHMTPGMKIYIDPPTYE	603
Db	550	LVSVSGSVVLVILLAAAFVIRRRSKYSKAKQEADEE-----KHLNGQVTVYDPTTYE	603
Qy	604	DNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKIFVAIKTLKSGYTEKQ	663
Db	604	DPQAVREFAKEIDASCIEKIVGGEFGEVCSGRLKVPKREICVAIKTLKAGYTDKQ	663
Qy	664	RDFLSEASIMQDPHPNVHLEGVVTSPTPMIITEFWNGSLDSFLRONDQFTVQL	723
Db	664	RRDFLSEASIMQDPHPNI IHLEGVVTVCKPVMIIITEFWNGSLDLAFLRKNDGRFTVQL	723
Qy	724	VGMLRGIAGMKYLAIDMNVVHRDLAARNILVNSNLVCKVSPFGLSRFLEDDTSDPTTSA	783
Db	724	VGMLRGIAGMKYLSMSVHRDLAARNILVNSNLVCKVSDFGMSRVLEDD-PEAAVYTR	782
Qy	784	LGKIPIRWTAPEATQYRKTSASDVWSYGIWVWEMVSGERYWDMVNTQDVINAIEDQY	843
Db	783	-GKIPIRWTAPEATYRKTSASDVWSYGIWVWEMVSGERYWDMVNTQDVINAIEDQY	841
Qy	844	RLPPPMDCSALHOLMDCQKRNHRPKFGQIVNTLDKMLRNPNLSKAMAPLSSGINLP	903
Db	842	RLPPPMDCPIALHQLMLDCQKERSDRPKFGQIVNMLDKLIRNPNLSKRTGTSSRPNTA	901
		Query Match	58.7%; Score 3045; DB 5; Length 986;
		Best Local Similarity	59.3%; Pred. No. 6.4e-218;
		Matches	580; Conservative 146; Mismatches 212; Indels 40; Gaps 12;
Qy	18	AVEETLMDSTTATAELGWMVHP-PSGWEVSGYDENMNTIRTYQVCNVFSSQNNWLRTK	76
Db	28	ANEVTLLDSRSVQELGWIASPLEGGWEVSIIMDEKNTPIRTYQVCNVMEPSQNNWLRTD	87
Qy	77	FIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSDATKTFPNWMENPVW	136
Db	88	WITREGARVVEIKFTLRDCNSLPFGYMGCKETFNLYYESDNDKERFI-----RENQFV	143
Qy	137	KVDITAADESFOVDLGRVNMKINTEVRSPGSKETFNLYYEADFDSDATKTFPNWMENPVW	196
Db	144	KIDITAADESFTQVDIGDRIMKLNTEIRDVGPLSKGFLAFQDVGACIALVSRVFYK	203
Qy	197	CPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGELWPIGRMC	256
Db	204	CPLTVRNLAQPPDITGADTSSLVEVRGSCVNNSEEDVP-KMYCGADGELWPIGNCLC	262
Qy	257	KAGFEAVENGIVCRGCPSGTFFKANQDEACTHCPINSRTTSEGATNCVCRNGYYRADLDP	316
Db	263	NAGHE--ERSGEQACKIGYKALSTDTATCAKCPHYSVWEGATSCDGRGFRADNDA	320
Qy	317	LDMPCTTIPSAQAVISSVNETSLMLETWTPRDSGGREDLVNIIKSCSG-RCGATRC	375
Db	321	ASMPCTPPSAPLNLISNNVNETSNLEWSSPQNTGGRQDISYNNVCKKCGAGDPKCRPC	380
Qy	376	GNVOYAPROGLTEPRIYISDLAHTQYTEIOAVNGVTDQSPSPQFASVNTNQAA	435
Db	381	GSQVHTPQNGLTKTKVTSITDLAHTNYTEIWAIVNGSVKYNPNPQSVSVTTNQAA	440
Qy	436	PSAVISMQHVSRTVDSITLSQSDQDPNGVILDYELQYKELSEYNATAIKSPNTNTVV	495
Db	441	PSSIALVQAEKTRYSVALAWLEDPDPNGVILEYEVKYEDQKQERSVIRVTAARNDI	500
Qy	496	QCLKAGAIYVQVARTVAGYCRVSGKMYFQMTAEAYQTSIQEKLK-LIIGS-----	547
Db	501	KGLNELTSYVPHVARTAAAGYDFSEPLEVTNT-----VPSRIIGDGANSTVL	549
Qy	548	--SAAGLVFLAVVIAVCHRR--GPERADSEYTDKLOHTSGHMTPGMKIYIDPPTYE	603
Db	550	LVSVSGSVVLVILLAAAFVIRRRSKYSKAKQEADEE-----KHLNGQVTVYDPTTYE	603
Qy	604	DNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKIFVAIKTLKSGYTEKQ	663
Db	604	DPQAVREFAKEIDASCIEKIVGGEFGEVCSGRLKVPKREICVAIKTLKAGYTDKQ	663
Qy	664	RDFLSEASIMQDPHPNVHLEGVVTSPTPMIITEFWNGSLDSFLRONDQFTVQL	723
Db	664	RRDFLSEASIMQDPHPNI IHLEGVVTVCKPVMIIITEFWNGSLDLAFLRKNDGRFTVQL	723
Qy	724	VGMLRGIAGMKYLAIDMNVVHRDLAARNILVNSNLVCKVSPFGLSRFLEDDTSDPTTSA	783
Db	724	VGMLRGIAGMKYLSMSVHRDLAARNILVNSNLVCKVSDFGMSRVLEDD-PEAAVYTR	782
Qy	784	LGKIPIRWTAPEATQYRKTSASDVWSYGIWVWEMVSGERYWDMVNTQDVINAIEDQY	843
Db	783	-GKIPIRWTAPEATYRKTSASDVWSYGIWVWEMVSGERYWDMVNTQDVINAIEDQY	841
Qy	844	RLPPPMDCSALHOLMDCQKRNHRPKFGQIVNTLDKMLRNPNLSKAMAPLSSGINLP	903
Db	842	RLPPPMDCPIALHQLMLDCQKERSDRPKFGQIVNMLDKLIRNPNLSKRTGTSSRPNTA	901

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Qy 376 GDNVOYAPROGLTEPRIYISDLIAHTOYTFEIOAVNGVTDQSPFPQFASVNIITNQAA 435
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
381 GSGVHYTPQONGLTKTTSITDLIAHTNYTFEIWAVNGSVKYNPNPDQSVSVTTTNQAA 440
Qy 436 PSVSIHQVSRVTVDSTLSQSDQDQNGVILDYLOVEKELSEYNATAIKSPTNVTV 495
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
441 PSSIALVOAKEVTRYSVLAWLEPDRPNGVILEYEVKYEKDQNERSYRIVRTAARNTDI 500
Qy 496 QGLKAGAIYVQVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPL-LIIGS----- 547
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
501 KGLNPLTSYVHFVARTAGYGFSEPLEVTTNT-----VPSRIIGDGANSTVL 549
Qy 548 --SAAGLVFLIAVVIAIVCNRR--GPERADSEYTDKLOHYTSCHMTPGMKIYIDPPTYE 603
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
550 LVSVSGSVLWVILIAAFVISRRRSKYSKAKQEADEE-----KHLNQGVRTYVDPPTYE 603
Qy 604 DPNKAEVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYTEKQ 663
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
604 DPNQAVREFAKEIDASCIEKIEKIVGGEFGEVCSGRUKVPGKREICVAIKTLKAGYTDKQ 663
Qy 664 RRDFLSEASIMGQDPHNVIIHLEGVVTCKSTPVMIIITBFMENGSLDSFLRQNDGQFTVIOL 723
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
664 RRDFLSEASIMGQDPHNVIIHLEGVVTCKSTPVMIIITBFMENGSLDAFLRKNDRGFTVIOL 723
Qy 724 VGMURGIAAGKYLADNMYVHRDLAARNILVNSLVCKVSDPGLSRFLEDDTSDPTVTS 783
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
724 VGMURGIGSGMKYLSMSYVHRDLAARNILVNSLVCKVSDPGLSRVLEDD-PEAAVYTR 782
Qy 784 LGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNODVINAIEQDY 843
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
783 -GGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMNSQDVIKABEY 841
Qy 844 RLPPPMDCPSALHQLMLDCWQDRNRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLP 903
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
842 RLPPPMDCPIALHQLMLDCWQXERSDRPKFGQIVNMLDKLIRNPNSLKRTCTESSRENTA 901
Qy 904 LLDRTPIDYTSFNTVDWLEAIKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLAGH 963
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
902 LLDPSPEFSVAVSGDWLQAIKMDRYKDNFTAAAGYTTLEAVVHVNQEDLARIGITAITH 961
Qy 964 QKKILNSIOVMRAQMNQI 981
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
962 QNKILSSVQAMRTQMOM 979

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Search completed: December 30, 2004, 16:51:35
Job time : 50 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 16:32:55 ; Search time 210 Seconds
(without alignments)
2701.521 Million cell updates/sec

Title: US-09-914-883-2
Perfect score: 5188
Sequence: 1 MALRRIGALLLLPLLAIVE.....ILNSIQVMRAQMNQIOSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5184	99.9	1055	1	EPB2_HUMAN
2	5168	99.6	1021	2	Q6GTQ7
3	5157.5	99.4	1029	2	Q6P5F1
4	5157.5	99.4	1029	2	AAH62924
5	5130	98.9	994	1	EPB2_MOUSE
6	4975.5	95.9	1004	1	EPB2_CHICK
7	4945	95.3	987	1	EPB2_COTUJA
8	3934.5	75.8	984	2	EPB1_RAT
9	3930.5	75.8	984	2	Q8CBF3
10	3924	75.6	984	1	EPB1_HUMAN
11	3916.5	75.5	984	2	Q6PG23
12	3916.5	75.5	984	2	AAH57301
13	3767	72.6	985	1	EPBA_XENLA
14	3753.5	72.3	815	2	O57458
15	3721	71.7	984	1	EPB1_CHICK
16	3705	71.4	943	2	Q8CB22
17	3670.5	70.7	998	2	Q7Z740
18	3662.5	70.6	998	1	EPB3_CHICK
19	3661.5	70.6	998	1	EPB3_HUMAN
20	3657.5	70.5	993	2	Q91Y59
21	3630.5	70.0	993	1	EPB3_MOUSE
22	3612.5	69.6	902	1	EPBB_XENLA
23	3489	67.3	974	2	Q6NR59
24	3489	67.3	974	2	AAH70804
25	3485	67.2	974	1	EPB3_XENLA
26	3480	67.1	974	2	Q6DFG4
27	3441	66.3	938	2	Q60669
28	3354.5	64.7	1002	1	EPB5_CHICK
29	3235	62.4	923	2	Q90ZN8
30	3085	59.5	986	1	EP4A_XENLA
31	3080	59.4	986	2	Q7ZYM7

ALIGNMENTS

32	3075.5	59.3	985	1	EP4B_XENLA
33	3065.5	59.1	986	1	EP4A_CHICK
34	3045	58.7	986	1	EP4A_HUMAN
35	3043	58.7	986	2	Q80VZ2
36	3040	58.6	986	1	EP4A_MOUSE
37	3038.5	58.6	993	1	EP47_CHICK
38	3036	58.5	1037	1	EP47_HUMAN
39	3028	58.4	998	1	EP47_HUMAN
40	3017	58.2	998	2	Q8BS08
41	3013	58.1	998	1	EP47_MOUSE
42	3013	58.1	998	1	EP47_RAT
43	3010.5	58.0	969	2	Q7Z3F2
44	3009	58.0	1013	1	EP45_CHICK
45	3006	57.9	994	2	Q8R381
46	2969	57.2	976	2	Q90ZN9
47	2959.5	57.0	927	2	Q99KA8
48	2931	56.5	983	1	EP43_CHICK
49	2930.5	56.5	983	1	EP43_HUMAN
50	2928	56.4	984	2	Q8BR81
51	2928	56.4	984	2	Q8C3U1
52	2925.5	56.4	983	2	Q6PAR6
53	2925.5	56.4	983	2	AAH63282
54	2923	56.3	1005	1	EP45_RAT
55	2914	56.2	984	1	EP43_RAT
56	2887.5	55.7	983	1	EP43_MOUSE
57	2863.5	55.2	987	2	Q99MR2
58	2860.5	55.1	987	2	Q8C7S3
59	2860	55.1	981	1	EP43_BRARE
60	2856.5	55.1	987	2	Q91YM0
61	2854.5	55.0	987	1	EP4A_MOUSE
62	2854	55.0	996	2	Q8C8K1
63	2844	54.8	987	1	EPB4_HUMAN
64	2844	54.8	987	2	AAL14194
65	2843.5	54.8	552	2	Q9H4H4
66	2843	54.8	987	2	Q7Z635
67	2839.5	54.7	621	2	Q9H4H3
68	2809.5	54.2	1035	1	EP46_MOUSE
69	2743.5	52.9	987	2	Q73875
70	2712.5	52.3	1005	1	EP48_HUMAN
71	2696.5	52.0	880	2	Q73879
72	2681	51.7	976	2	Q73878
73	2674	51.5	1004	1	EP48_MOUSE
74	2654	51.2	935	2	Q96L35
75	2599.5	50.1	948	1	EP46_RAT
76	2545	49.1	482	2	Q6NVM1
77	2545	49.1	482	2	AAH67861
78	2485.5	47.9	864	2	Q6KF80
79	2467	47.6	1014	2	Q8K0A9
80	2465	47.5	1014	2	Q8BN76
81	2464	47.5	877	1	EP45_MOUSE
82	2463	47.5	1014	1	EP46_MOUSE
83	2461	47.4	1006	1	EP46_HUMAN
84	2461	47.4	1006	2	AAH20939
85	2391	46.1	819	2	Q6PFV6
86	2391	46.1	819	2	AAH57401
87	2389.5	46.1	818	2	Q6KF79
88	2370.5	45.7	976	2	Q8N3Z2
89	2357	45.4	977	1	EP42_MOUSE
90	2356.5	45.4	976	1	EP42_HUMAN
91	2343.5	45.2	974	2	Q6DI14
92	2318.5	44.7	976	2	Q6NTV5
93	2318.5	44.7	976	2	AAH68849
94	2313.5	44.6	977	2	Q9PWR5
95	2272.5	43.8	1011	2	Q6VU50
96	2272.5	43.8	1011	2	AAQ87231
97	2236	43.1	984	2	Q6NZS1
98	2236	43.1	984	2	AAH65990
99	2069	39.9	1003	2	Q95YL0
100	2051.5	39.5	969	2	Q98TD0

RESULT 1
 EPB2_HUMAN
 ID EPB2_HUMAN STANDARD; PRT; 1055 AA.
 AC P29323; O43477;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HEK5
 DE (ERK)).
 GN Name=EPHB2; Synonyms=EPTB3, ERK, DRT, HEK5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Fetal brain;
 RX MEDLINE=96154673; PubMed=8589679;
 RA Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C., Yoshioka A.,
 RA Sulman E.P., Brodeur G.M., Pleasure D.E.;
 RT "Molecular characterization and chromosomal localization of DRT
 RT (EPH3): a developmentally regulated human protein-tyrosine kinase
 RT gene of the EPH family.";
 RL Hum. Mol. Genet. 4:2033-2045(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Gastric carcinoma;
 RX MEDLINE=93343925; PubMed=7688222;
 RA Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;
 RA "Identification of protein-tyrosine kinase genes preferentially
 RA expressed in embryo stomach and gastric cancer.";
 RL Biochem. Biophys. Res. Commun. 194:698-705(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Fetal brain;
 RX MEDLINE=98359217; PubMed=9696046;
 RA Tang X.X., Pleasure D.E., Brodeur G.M., Ikegaki N.;
 RA "A variant transcript encoding an isoform of the human protein
 RA tyrosine kinase EPHB2 is generated by alternative splicing and
 RA alternative use of polyadenylation signals.";
 RL Oncogene 17:521-526(1998).
 RN [4]
 RP SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Brain;
 RX MEDLINE=95206782; PubMed=7898931;
 RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
 RA Basu R., Welcher A.A.;
 RT "cDNA cloning and tissue distribution of five human EPH-like receptor
 RT protein-tyrosine kinases.";
 RL Oncogene 10:897-905(1995).
 RN [5]
 RP SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Fetal brain;
 RX PubMed=7601466;
 RA Saito T., Seki N., Mateuda Y., Kitahara M., Murata M., Kanda N.,
 RA "Identification of the human ERK gene as a putative receptor tyrosine
 RA kinase and its chromosomal localization to lp36.1: a comparative
 RA mapping of human, mouse, and rat chromosomes.";
 RL Genomics 26:382-384(1995).
 RN [6]
 RP SEQUENCE OF 652-712 FROM N.A.
 RX MEDLINE=91296384; PubMed=1648701;
 RA Chan J., Watt V.M.;
 RT "eek and erk, new members of the eph subclass of receptor protein-
 RT tyrosine kinases.";
 RL Oncogene 6:1057-1061(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).
 RX MEDLINE=99132419; PubMed=993164;
 RA Thomas C.D., Goodwill K.E., Bowie J.U.;

"Oligomeric structure of the human EphB2 receptor SAM domain.";
 Science 283:833-836(1999).
 CC -1- FUNCTION: Receptor for members of the ephrin-B family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: The ligand-activated form interacts with multiple
 CC proteins, including GTPase-activating protein (RASGAP) through its
 CC SH2 domain. Binds RASGAP through the juxtamembrane tyrosines
 CC residues. Interacts with PRKCBP and GRIP1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=Long; Synonyms=EPHB2V;
 CC IsoId=P29323-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P29323-2; Sequence=VSP_003016, VSP_003017;
 CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta,
 CC pancreas, liver and skeletal muscle. Preferentially expressed in
 CC fetal brain.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; L41939; AAA99310.1; -;
 CC EMBL; D31661; BAA06506.1; -;
 CC EMBL; AF025304; AAB94602.1; -;
 CC EMBL; D14717; BAA03537.1; -;
 CC EMBL; L36643; AAA74244.1; -;
 CC EMBL; D37827; BAA07073.1; -;
 CC EMBL; X59292; CAA41981.1; -;
 CC PIR; A57174; A57174.
 CC PDB; 1B4F; X-ray; A/B/C/D/E/F/G/H=-.
 CC PDB; 1F0W; X-ray; A=905-986.
 CC Genew; HGNC:3393; EPHB2.
 CC MIM; 600997; -;
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005005; P:transmembrane-ephrin receptor activity; TAS.
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR001090; Ephrin receptor.
 CC InterPro; IPR003962; FIII subd.
 CC InterPro; IPR003961; FN III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR008979; Gal_bind like.
 CC InterPro; IPR011009; Kinase like.
 CC InterPro; IPR00719; Prot kinase.
 CC InterPro; IPR001660; SAM_
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR008266; Tyr_kinase AS.
 CC InterPro; IPR001426; YKase_receptor.
 CC Pfam; PF01404; Ephrin_lbd; 1.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00069; Pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD001495; Ephrin_receptor; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00615; EPH_lbd; 1.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00454; SAM; 1.
 CC SMART; SM00219; TYRK; 1.
 CC PROSITE; PS01186; EGF_2; 1.

DR	PROSITE; PS00853; FN3; 2.	
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.	
DR	PROSITE; PS00109; PROTEIN KINASE TYR; 1.	
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V1; 1.	
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V2; 1.	
DR	PROSITE; PS00105; SAM_DOMAIN; 1.	
KW	3D-structure; Alternative splicing; ATP-binding; Glycoprotein; phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.	
KW	Tyrosine-protein kinase.	
FT	SIGNAL 1 18	Potential.
FT	CHAIN 19 1055	Ephrin type-B receptor 2.
FT	DOMAIN 19 543	Extracellular (Potential).
FT	TRANSMEM 544 564	Potential.
FT	DOMAIN 565 1055	Cytoplasmic (Potential).
FT	DOMAIN 184 324	Cys-rich.
FT	DOMAIN 325 426	Fibronectin type-III 1.
FT	DOMAIN 432 527	Fibronectin type-III 2.
FT	DOMAIN 621 884	Protein kinase.
FT	DOMAIN 913 977	SAM.
FT	SITE 984 986	PDZ-BINDING MOTIF (IN SHORT ISOFORM) (POTENTIAL).
FT	NP_BIND 627 635	ATP (By similarity).
FT	BINDING 653 653	ATP (By similarity).
FT	ACT_SITE 746 746	By similarity.
FT	MOD_RES 596 596	Phosphotyrosine (by autocatalysis) (Potential).
FT	MOD_RES 602 602	Phosphotyrosine (by autocatalysis) (Potential).
FT	MOD_RES 780 780	Phosphotyrosine (by autocatalysis) (Potential).
FT	MOD_RES 930 930	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CARBOHYD 265 265	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 336 336	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 428 428	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD 482 482	N-linked (GlcNAc. .) (Potential).
FT	VARSPLIC 986 986	G -> V (in isoform Short).
FT	VARSPLIC 987 1055	/FTid=VSP_003016.
FT	VARIANT 671 671	Missing (in isoform Short).
FT	CONFLICT 1 20	/FTid=VSP_003017.
FT	CONFLICT 154 154	A -> R.
FT	CONFLICT 476 476	/FTid=VAR_004162.
FT	CONFLICT 495 495	MALRRGALLPLLAEE -> MWVPLALPVCTVA (in Ref. 2).
FT	CONFLICT 532 532	G -> D (in Ref. 2).
FT	CONFLICT 568 568	K -> Q (in Ref. 2).
FT	CONFLICT 589 589	Missing (in Ref. 4).
FT	CONFLICT 788 788	E -> D (in Ref. 2).
FT	CONFLICT 853 853	R -> RR (in Ref. 1).
FT	CONFLICT 923 923	M -> I (in Ref. 4).
FT	CONFLICT 956 956	I -> F (in Ref. 4).
FT	CONFLICT 958 958	S -> A (in Ref. 2 and 5).
FT	HELIX 918 924	E -> K (in Ref. 2 and 5).
FT		L -> V (in Ref. 3 and 5).
FT		V -> L (in Ref. 1).
Query Match 99.9%; Score 5184; DB 1; Length 1055;		
Best Local Similarity 100.0%; Pred. No. 2e-315; Indels 0; Gaps 0;		
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MALRRGALLPLLAEEETLMDSTATAELGMMVHPSPGSGEVSVDENMTIRTYQ 60
Db	1	MALRRGALLPLLAEEETLMDSTATAELGMMVHPSPGSGEVSVDENMTIRTYQ 60
Qy	61	VCNVFESSQNNWLTKFIRRRGAHRIHVEKMFVRDCSSIPSPGSKCTFNLYYEADF 120
Db	61	VCNVFESSQNNWLTKFIRRRGAHRIHVEKMFVRDCSSIPSPGSKCTFNLYYEADF 120
Qy	121	DSATKTPNNWENPWKVDITADESFQVDLGGVNMKINTEVRSFGVPSRSGFYLAQD 180
Db	121	DSATKTPNNWENPWKVDITADESFQVDLGGVNMKINTEVRSFGVPSRSGFYLAQD 180

Qy	181	YGCMSLIAVRVFRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db	181	YGCMSLIAVRVFRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Qy	241	CNGDGWLVPIGRCMKAGFEAVENGTVCRGCSGTFKANKQGBEACTHCHINSRTTSEGA 300
Db	241	CNGDGWLVPIGRCMKAGFEAVENGTVCRGCSGTFKANKQGBEACTHCHINSRTTSEGA 300
Qy	301	TNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLBWTTPRDSGGREDLVYNI 360
Db	301	TNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLBWTTPRDSGGREDLVYNI 360
Qy	361	ICKSCSGRGACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQVTFEIQAVNGVTDQSPF 420
Db	361	ICKSCSGRGACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQVTFEIQAVNGVTDQSPF 420
Qy	421	SPOFASVNITTTQAAPSAVSIMHQSRTVDSITLSWSQDPDPNGVILDYLOEYKELSE 480
Db	421	SPOFASVNITTTQAAPSAVSIMHQSRTVDSITLSWSQDPDPNGVILDYLOEYKELSE 480
Qy	481	YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFOTMTAEAYQTSIQEK 540
Db	481	YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFOTMTAEAYQTSIQEK 540
Qy	541	LPLIIGSSAAGLVFLIAVVVIAIVCNRGRPERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Db	541	LPLIIGSSAAGLVFLIAVVVIAIVCNRGRPERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Qy	601	TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660
Db	601	TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660
Qy	661	EKORRDFLSEASIMGQFDHPNVTHLEGVTKSPVPMIITEFMENGLSDSLRQNDGQFTV 720
Db	661	EKORRDFLSEASIMGQFDHPNVTHLEGVTKSPVPMIITEFMENGLSDSLRQNDGQFTV 720
Qy	721	IQLVGLRGIAAGMKYLADNMYVHRDLAARNILVNSNLCKVSDPGLSRFLEDDTSDPTY 780
Db	721	IQLVGLRGIAAGMKYLADNMYVHRDLAARNILVNSNLCKVSDPGLSRFLEDDTSDPTY 780
Qy	781	TSALGGKIPIRWTAPAIQYRKETSADVWSYGIWMVMSYGERPYWDMTNDQVINAIE 840
Db	781	TSALGGKIPIRWTAPAIQYRKETSADVWSYGIWMVMSYGERPYWDMTNDQVINAIE 840
Qy	841	QDYRLPPMDPCPSALHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNSLKANAPLSSGI 900
Db	841	QDYRLPPMDPCPSALHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNSLKANAPLSSGI 900
Qy	901	NLPFLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSQMMEDILRLGVTL 960
Db	901	NLPFLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSQMMEDILRLGVTL 960
Qy	961	AGHOKILANSIQWRAQMNIQISVE 985
Db	961	AGHOKILANSIQWRAQMNIQISVE 985
RESULT 2		
Q6GTQ7 PRELIMINARY; PRT; 1021 AA.		
ID	Q6GTQ7	AC
DT	05-JUL-2004 (T-EMBLrel. 27, Created)	Q6GTQ7;
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)	DT
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)	DT
DE	Ephb2 protein (Fragment).	DE
GN	Name=Ephb2;	GN
OS	Mus musculus (Mouse).	OS
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	OC
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	OC
OX	NCBI_TaxID=10090;	OX
RN	[1]	RN
RP	SEQUENCE FROM N.A.	RP

RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 FT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 DR EMBL; BC043088; AAH43088.1; -;
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR01090; Ephrin_receptor.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal_bind like.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR011510; SAM 2.
 DR InterPro; IPR010993; SAM_homology.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase AS.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM_1; 1.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR ProDom; PD00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrcK; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 FT NON_TER 1

SQ	SEQUENCE	1021 AA;	113271 MW;	2BA741083DEC6164 CRC64;
Query Match	99.6%;	Score 5168;	DB 2;	Length 1021;
Best Local Similarity	99.4%;	Pred. No. 2e-314;	1;	Indels 0; Gaps 0;
Matches 980;	Conservative	5;	Mismatches	1;
QY	1	MALRRLLGALLLLPLLA	VEETLMDSTTATAEL	GMVHPHPPSGWEEVSGYDENNTIRTYQ 60
DB	36	MAVRRLLGALLLLPLLA	VEETLMDSTTATAEL	GMVHPHPPSGWEEVSGYDENNTIRTYQ 95
QY	61	VGNVFSSQNNWLRTKFI	RRRGAHR IHVEMKFSVR	DCSSIPSPVSGCKETFNLYYEADF 120
DB	96	VGNVFSSQNNWLRTKFI	RRRGAHR IHVEMKFSVR	DCSSIPSPVSGCKETFNLYYEADF 155
QY	121	DSATKTFPNMNPWKVDT	IADESFQVLDLGRVKN	INTEVRSFGPVSRSFYLAQD 180
DB	156	DLATKTFPNMNPWKVDT	IADESFQVLDLGRVKN	INTEVRSFGPVSRSFYLAQD 215
QY	181	YGGCMLIAVRVFRYKCP	RIIONGAIFQETLSGA	ESTSLVAARGSCIANAEVDVPIKLY 240
DB	216	YGGCMLIAVRVFRYKCP	RIIONGAIFQETLSGA	ESTSLVAARGSCIANAEVDVPIKLY 275
QY	241	CNGDGEWLVPIGRCMCK	AGFEAVENGTVCRGCP	SGTFFKANQGDCACTHCPINRRTTSEGA 300
DB	276	CNGDGEWLVPIGRCMCK	AGFEAVENGTVCRGCP	SGTFFKANQGDCACTHCPINRRTTSEGA 335
QY	301	TNCVCBNGYVRADLDPL	DMPTTIPSAPOAVISS	VNNTSILMLEWTPPRDSGGREDLVYNI 360
DB	336	TNCVCBNGYVRADLDPL	DMPTTIPSAPOAVISS	VNNTSILMLEWTPPRDSGGREDLVYNI 395
QY	361	ICKSCSGRGACVRCGDN	VQYAPROLGLTEPRI	YISDLLAHTQYTFEIQAVNGVTDQSPF 420
DB	396	ICKSCSGRGACVRCGDN	VQYAPROLGLTEPRI	YISDLLAHTQYTFEIQAVNGVTDQSPF 455
QY	421	SPOFASVNTTNOAAPS	SAVSIMHOVSRVDSIT	LSWSQDPQNGVILDELYEYKELSE 480
DB	456	SPOFASVNTTNOAAPS	SAVSIMHOVSRVDSIT	LSWSQDPQNGVILDELYEYKELSE 515
QY	481	YNATAIKSPNTVTVOGL	KAGAIYVFOVRARTV	AGYGRYSGKMYFOTMTEAEYQTSIOEK 540
DB	516	YNATAIKSPNTVTVOGL	KAGAIYVFOVRARTV	AGYGRYSGKMYFOTMTEAEYQTSIOEK 575
QY	541	LPLIGSSAAGLVFLIA	VVIAIVCNRRGFERA	DSEYTDKLOHYTSGHMTPGMKIYIDPF 600
DB	576	LPLIGSSAAGLVFLIA	VVIAIVCNRRGFERA	DSEYTDKLOHYTSGHMTPGMKIYIDPF 635
QY	601	TYEDPNEAVREPAKEI	DISCVKIEQIVIGAGE	FGVCSGHLKLPCKREIFVAIKTLKSGYT 660
DB	636	TYEDPNEAVREPAKEI	DISCVKIEQIVIGAGE	FGVCSGHLKLPCKREIFVAIKTLKSGYT 695
QY	661	EKORRDFLSEASIMGO	FDHPNVTHLGVVTK	SPVMIITFEFMNGSLDSFLRQNDGQFTV 720
DB	696	EKORRDFLSEASIMGO	FDHPNVTHLGVVTK	SPVMIITFEFMNGSLDSFLRQNDGQFTV 755
QY	721	IQLVGMRLGIAAGMKY	LADNMYVHRDLAARN	ILVNSNLCKVSDFGLSRLEDDTSDPTY 780
DB	756	IQLVGMRLGIAAGMKY	LADNMYVHRDLAARN	ILVNSNLCKVSDFGLSRLEDDTSDPTY 815
QY	781	TSALGGKIPIRWTAPA	EAIQYRKFTSADVWS	YIGIVMWEVMSYGERPYWDNTQDVINAIE 840
DB	816	TSALGGKIPIRWTAPA	EAIQYRKFTSADVWS	YIGIVMWEVMSYGERPYWDNTQDVINAIE 875
QY	841	QDYRLPPPMDCPSALH	QMLDMCDKQDRNHR	PKFGQIVNTLDMKIRNPNSLKAPLSSGI 900
DB	876	QDYRLPPPMDCPSALH	QMLDMCDKQDRNHR	PKFGQIVNTLDMKIRNPNSLKAPLSSGI 935
QY	901	NLPLLDRTTIPDYTS	FNFTVDEWLEAIKMG	QYKESFANAGFTSFVDVQSOMMEDILRLGVTL 960
DB	936	NLPLLDRTTIPDYTS	FNFTVDEWLEAIKMG	QYKESFANAGFTSFVDVQSOMMEDILRLGVTL 995
QY	961	AGHQKILANSIQWMRA	QMNIQISVEV 986	
DB	996	AGHQKILANSIQWMRA	QMNIQISVEV 1021	

RESULT 3
Q6P5F1 PRELIMINARY; PRT; 1029 AA.

AC Q6P5F1, 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ephb2 protein (Fragment).
GN Name=Ephb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strauberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
receptor subfamily.
DR EMBL; BC062924; AAH62924.1; -.
DR GO; GO:0008046; P:axon guidance receptor activity; IDA.
DR GO; GO:0005003; P:ephrin receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0005102; F:receptor binding; IDA.
DR GO; GO:0007411; P:axon guidance; IDA.
DR GO; GO:0007612; P:learning; IMP.
DR GO; GO:0048170; P:positive regulation of long-term neuronal s...; IMP.
DR GO; GO:0048168; P:regulation of neuronal synaptic plasticity; IMP.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind-like.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR InterPro; IPR010993; SAM_homology.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase AS.
DR InterPro; IPR001426; Ykase_receptorv.

DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM_1; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00853; FN3_2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00730; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW transferase; Transmembrane; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 1029 AA; 114282 MW; A920A28E4A9A93BA CRC64;

Query Match 99.4%; Score 5157.5; DB 2; Length 1029;
Best Local Similarity 99.3%; Pred. No. 9e-314; Indels 1; Gaps 1;
Matches 980; Conservative 5; Mismatches 1;

QY 1 MALRLRGAALLLLPLLAAVEETLMDSTATAELGWMVHPSPGWEVSGYDENNTIRTYQ 60
DB 43 MAVRLRGAALLLLPLLAAVEETLMDSTATAELGWMVHPSPGWEVSGYDENNTIRTYQ 102

QY 61 VCNVFESSQNWLRTKFIKRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120
DB 103 VCNVFESSQNWLRTKFIKRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 162

QY 121 DSATKTFNNMNPWKVDITIADESFSQVDLGRVKNKINTEVRSFGPVSRSFYLAQD 180
DB 163 DLATKTFNNMNPWKVDITIADESFSQVDLGRVKNKINTEVRSFGPVSRSFYLAQD 222

QY 181 YGCMSLIAVRVYRKPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
DB 223 YGCMSLIAVRVYRKPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLY 282

QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINRTTSEGA 300
DB 283 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINRTTSEGA 342

QY 301 TNCVCRNGYRADLDPDMPCTTIPAPQAVISSVNETSLMLEWTPPRDSGGREDLYVNI 360
DB 343 TNCVCRNGYRADLDPDMPCTTIPAPQAVISSVNETSLMLEWTPPRDSGGREDLYVNI 402

QY 361 ICKSCSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPF 420
DB 403 ICKSCSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPF 462

QY 421 SPQFASVNTTNOAAPSIVMSHQSRTVDSITLSWSQDPQDPNGVILDYELQYKEL-ELS 479
DB 463 SPQFASVNTTNOAAPSIVMSHQSRTVDSITLSWSQDPQDPNGVILDYELQYKEL-ELS 522

QY 480 EYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGRYGKGYQTMTEAEYQTSIQE 539
DB 523 EYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGRYGKGYQTMTEAEYQTSIQE 582

QY 540 KLPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTPGMKIYIDP 599
DB 583 KLPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTPGMKIYIDP 642

QY 600 FTYEDPNEAVREPFAKSIDISCVKIEQVIGAGEFGEVCSGHLKLPKGRFIVAIAIKLSGY 659

Db 643 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGY 702
QY
Db 660 TEKORRDFLSEASIMGQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLQNDGQFT 719
QY
Db 703 TEKORRDFLSEASIMGQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLQNDGQFT 762
QY
Db 720 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPT 779
Db 763 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPT 822
QY
Db 780 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVWSYGIWVMEVMSYGERPYDMTQDVINAI 839
Db 823 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVWSYGIWVMEVMSYGERPYDMTQDVINAI 882
QY
Db 840 EODYRLPPMPCDPSALHQLMDCWKQDNRHPRKFGQIVNTLDKMRNPNSLKAMAPLSSG 899
Db 883 EODYRLPPMPCDPSALHQLMDCWKQDNRHPRKFGQIVNTLDKMRNPNSLKAMAPLSSG 942
QY
Db 900 INPLLDRTTIPDYTSFNTVDEWLEAIKWQYKESFANAGFTSFVWSQMMEDILRLGVT 959
Db 943 INPLLDRTTIPDYTSFNTVDEWLEAIKWQYKESFANAGFTSFVWSQMMEDILRLGVT 1002
QY
Db 960 LAGHOKILNSIQVMRAQMNQIQSVEV 986
Db 1003 LAGHOKILNSIQVMRAQMNQIQSVEV 1029
RESULT 4
AAH62924 PRELIMINARY; PRT; 1029 AA.
ID AAH62924
AC AAH62924;
DC 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ephb2 protein (Fragment).
GN EPHB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC062924; AAH62924.1; -;
FT NON TER 1
SQ SEQUENCE 1029 AA; 114282 MW; A920A28E4A9A93BA CRC64;

Query Match 99.4%; Score 5157.5; DB 2; Length 1029;
Best Local Similarity 99.3%; Pred. No. 9e-314;
Matches 980; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
QY 1 MALRLRGAALLLLPILAAVEETLMDSTTATAELGVMVHPSPGWEESYGVYDENNTIRTYQ 60
Db 43 MAVRRLGAALLLLPILAAVEETLMDSTTATAELGVMVHPSPGWEESYGVYDENNTIRTYQ 102
QY 61 VCNVFESSQNNMLRTKFIIRRRGAHRHIVEMKESVRDCSSIPSPGSCKETFNLYYYEADF 120
Db 103 VCNVFESSQNNMLRTKFIIRRRGAHRHIVEMKESVRDCSSIPSPGSCKETFNLYYYEADF 162
QY 121 DSATKTFPNMNMENPWKVDITIAADESFQVDLGGRVKMKINTEVRSFGPVSRSFYLAQD 180
Db 163 DLATKTFPNMNMENPWKVDITIAADESFQVDLGGRVKMKINTEVRSFGPVSRSFYLAQD 222
QY 181 YGCGMSLIAVRVYRCPRIIQNGAIFOETLSAESTSLVAARGSCIANAEVDVPIKLY 240
Db 223 YGCGMSLIAVRVYRCPRIIQNGAIFOETLSAESTSLVAARGSCIANAEVDVPIKLY 282
QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300
Db 283 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINSRTTSEGA 342
QY 301 TNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRSGGREDLVYNI 360
Db 343 TNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRSGGREDLVYNI 402
QY 361 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 420
Db 403 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 462
QY 421 SPOFASVNTTNOAPSASVIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYEEK-ELS 479
Db 463 SPOFASVNTTNOAPSASVIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYEEKELS 522
QY 480 EYNATAIKPSTNTVTVOGLKAGAIYVQVRARTVAGRYGSGYQWYFQTMTEABYQTSIQE 539
Db 523 EYNATAIKPSTNTVTVOGLKAGAIYVQVRARTVAGRYGSGYQWYFQTMTEABYQTSIKE 582
QY 540 KLPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTGPKKIYIDP 599
Db 583 KLPLIVGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTGPKKIYIDP 642
QY 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGY 659
Db 643 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGY 702
QY 660 TEKORRDFLSEASIMGQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLQNDGQFT 719
Db 703 TEKORRDFLSEASIMGQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLQNDGQFT 762
QY 720 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPT 779
Db 763 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLSDTSDPT 822
QY 780 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVWSYGIWVMEVMSYGERPYDMTQDVINAI 839
Db 823 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVWSYGIWVMEVMSYGERPYDMTQDVINAI 882
QY 840 EODYRLPPMPCDPSALHQLMDCWKQDNRHPRKFGQIVNTLDKMRNPNSLKAMAPLSSG 899
Db 883 EODYRLPPMPCDPSALHQLMDCWKQDNRHPRKFGQIVNTLDKMRNPNSLKAMAPLSSG 942
QY 900 INPLLDRTTIPDYTSFNTVDEWLEAIKWQYKESFANAGFTSFVWSQMMEDILRLGVT 959
Db 943 INPLLDRTTIPDYTSFNTVDEWLEAIKWQYKESFANAGFTSFVWSQMMEDILRLGVT 1002
QY 960 LAGHOKILNSIQVMRAQMNQIQSVEV 986
Db 1003 LAGHOKILNSIQVMRAQMNQIQSVEV 1029

FT	MOD_RES	788	788	(Potential). Phosphotyrosine (by autocatalysis)
FT	MOD_RES	938	938	(Potential). Phosphotyrosine (by autocatalysis) (By similarity).
FT	DISULFID	70	192	
FT	DISULFID	105	115	
FT	CARBOHYD	273	273	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	344	344	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	436	436	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	490	490	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	576	576	R -> RR (in Ref. 2).
SEQ	SEQUENCE	994 AA;	110759 MW;	BC6B9B12A070394C CRC64;
Query Match. 98.9%; Score 5130; DB 1; Length 994;				
Best Local Similarity 99.5%; Pred. No. 4.5e-312;				
Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
Qy	10	LLLLPLLA	VEETLMDSTTAAELGWMVHPSPSGWEEVSGYDENMNTIRTYQVNCVFFSSQ	69
Db	18	LLLLPLLA	VEETLMDSTTAAELGWMVHPSPSGWEEVSGYDENMNTIRTYQVNCVFFSSQ	77
Qy	70	NNMLRTKFI	RRRGARRIHVEMKFSVRDCSSIPSPVSGCKETFNNIYYEADPDSATKTFPN	129
Db	78	NNMLRTKFI	RRRGARRIHVEMKFSVRDCSSIPSPVSGCKETFNNIYYEADPDLATKTFPN	137
Qy	130	WMENPWVKV	DTIADESPQVDLGGRYMKINTEVRSFGPVSRSGFYLAFOYGGCMLIA	189
Db	138	WMENPWVKV	DTIADESPQVDLGGRYMKINTEVRSFGPVSRSGFYLAFOYGGCMLIA	197
Qy	190	VRVYRKPRII	QNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL	249
Db	198	VRVYRKPRII	QNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL	257
Qy	250	PIGRCMCKAG	PEAVENGTVCRGCSGTFKANQGEACTHCIPNSRTTSEGNATNCVRNGY	309
Db	258	PIGRCMCKAG	PEAVENGTVCRGCSGTFKANQGEACTHCIPNSRTTSEGNATNCVRNGY	317
Qy	310	YRADLDPLDM	ECTTIPSAPOQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR	369
Db	318	YRADLDPLDM	ECTTIPSAPOQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR	377
Qy	370	GACTRCGNVQ	YAPRLGLTTPRIYISDLAHTQYTFEIQAVNGVTDOSPSPQFASVNI	429
Db	378	GACTRCGNVQ	YAPRLGLTTPRIYISDLAHTQYTFEIQAVNGVTDOSPSPQFASVNI	437
Qy	430	TTNQAPSAVSI	MQVSRVDSITLSWSQPQNGVILDYELQYKEKELSEYNATAIKSP	489
Db	438	TTNQAPSAVSI	MQVSRVDSITLSWSQPQNGVILDYELQYKEKELSEYNATAIKSP	497
Qy	490	TNTVTVOGL	KAGAIYVFOVRTAVAGYGRYSGKMYFTQWTAEBYOTSIOEKLPLIIGSSA	549
Db	498	TNTVTVOGL	KAGAIYVFOVRTAVAGYGRYSGKMYFTQWTAEBYOTSIOEKLPLIIGSSA	557
Qy	550	AGLVFLIAV	VIACVNRGRGERADSEYTKLOHYTSGHMPGMKIYIDDPFYEDPNEAV	609
Db	558	AGLVFLIAV	VIACVNRGRGERADSEYTKLOHYTSGHMPGMKIYIDDPFYEDPNEAV	617
Qy	610	REFAKEIDIS	CVKIEQVIGAGEFVGCVSHLKLPGKREIFVAIKTLKSGYTEKQRDFLS	669
Db	618	REFAKEIDIS	CVKIEQVIGAGEFVGCVSHLKLPGKREIFVAIKTLKSGYTEKQRDFLS	677
Qy	670	EASIMGQF	DPHPNVIHLEGVVTKSTPMIITEPMENGSLDSFLRQNDGQFTVIQLVGMRLG	729
Db	678	EASIMGQF	DPHPNVIHLEGVVTKSTPMIITEPMENGSLDSFLRQNDGQFTVIQLVGMRLG	737
Qy	730	IAAGMKYL	ADNMVYHRDLAARNILVNSNLVKCVSDFLGSRFLEDDTSDPTYSALGGKIP	789
Db	738	IAAGMKYL	ADNMVYHRDLAARNILVNSNLVKCVSDFLGSRFLEDDTSDPTYSALGGKIP	797
Qy	790	IRWTAPEAI	QVRKFTSASDVNSYIGIVMVEWMSYGERPYWDMTNQDVINAIEQDYRLPPPM	849
Db	798	IRWTAPEAI	QVRKFTSASDVNSYIGIVMVEWMSYGERPYWDMTNQDVINAIEQDYRLPPPM	857

DR EMBL; M62325; AAA48667.1; ALT_INIT.
 DR PDB; 1SGG; NMR; @=924-998.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN III-like.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal_bind like.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; TRYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS0853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW 3D-structure; Alternative splicing; ATP-binding; Glycoprotein;
 KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1004 Ephrin type-B receptor 2.
 FT DOMAIN 20 544 Extracellular (Potential).
 FT TRANSMEM 545 565 Potential.
 FT DOMAIN 566 1004 Cytoplasmic (Potential).
 FT DOMAIN 20 321 Cys-rich.
 FT DOMAIN 326 427 Fibronectin type-III 1.
 FT DOMAIN 433 528 Fibronectin type-III 2.
 FT DOMAIN 639 902 Protein kinase.
 FT DOMAIN 931 995 SAM.
 FT SITE 1002 1004 PDZ-binding motif (Potential).
 FT NP_BIND 645 653 ATP (By similarity).
 FT BINDING 671 671 ATP (By similarity).
 FT ACT_SITE 764 764 By similarity.
 FT MOD_RES 614 614 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 620 620 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 798 798 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 948 948 Phosphotyrosine (by autocatalysis) (By similarity).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 429 429 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 478 478 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 591 606 Missing (in isoform Short).
 FT TURN 931 932 /FTId=VSP_003018.
 FT HELIX 936 942
 FT TURN 943 944
 FT HELIX 946 948
 FT HELIX 949 955
 FT TURN 956 956
 FT TURN 960 961

FT HELIX 962 965
 FT HELIX 968 974
 FT TURN 975 975
 FT TURN 979 980
 FT HELIX 981 995
 SQ SEQUENCE 1004 AA; 111963 MW; 8D26213970ECC6E0 CRC64;
 Query Match 95.9%; Score 4975.5; DB 1; Length 1004;
 Best Local Similarity 94.3%; Pred. No. 2.1e-302;
 Matches 937; Conservative 28; Mismatches 12; Indels 17; Gaps 2;
 Qy 10 LLLPLLAABVEETLMDSTTATAGLWVHPSPGHEEVSVDENNTTIRTVQVCNVFESSQ 69
 Db 11 LALLPLLAABVEETLMDSTTATAGLWVHPSPGHEEVSVDENNTTIRTVQVCNVFESSQ 70
 Qy 70 NNWLRTKFIIRRGAAHRIHVEMKFSVRDSSIPSPVPGSKETFNLYYEADFDSATKTFPN 129
 Db 71 NNWLRTKYIIRRGAAHRIHVEMKFSVRDSSIPNPVPGSKETFNLYYEFDFDSATKTFPN 130
 Qy 130 WMENPMVKVDITIAADESFSQVDLGGRVKMKINTEVRSFGVSRSGFYLAFOGYGCMSLIA 189
 Db 131 WMENPMVKVDITIAADESFSQVDLGGRVKMKINTEVRSFGVSRSGFYLAFOGYGCMSLIA 190
 Qy 190 VRVYRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
 Db 191 VRVYRKCPRIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 250
 Qy 250 PIGRCMKAGFEAVENGTCVRCGCPSTFKANQGDGDEACTHCPINSRTTSEGATNCVCRNGY 309
 Db 251 PIGRCMCPGYESVENGTVCRCGCPSTFKASQDDEGCVHCPINSRTTSEGATNCVCRNGY 310
 Qy 310 YRADLDPDMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369
 Db 311 YRADAPVDMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 370
 Qy 370 GACTRCGDNVQAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 429
 Db 371 GACTRCGDNVQAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 430
 Qy 430 TTNOAAPSASVIMHOVSRTVDSITLWSQDPQPNVLDYELQYKELESEYNATAIKSP 489
 Db 431 TTNOAAPSASVIMHOVSRTVDSITLWSQDPQPNVLDYELQYKELESEYNATAIKSP 490
 Qy 490 TMTVTVOGLKAGAIYVQVREARTVAGYGRYSGRMVFTQMTAEAYQTSIQBKPLIIGSSA 549
 Db 491 TMTVTVOGLKAGAIYVQVREARTVAGYGRYSGRMVFTQMTAEAYQTSIQBKPLIIGSSA 550
 Qy 550 AGLVFLIAVVVIAVCN-RRGFERADSEYTDKLOHTYSGH-----MTPG 592
 Db 551 AGLVFLIAVVVIAVCN-RRGFERADSEYTDKLOHTYSGH-----MTPG 610
 Qy 593 MKIYIDPFTVEDNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAI 652
 Db 611 MKIYIDPFTVEDNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAI 670
 Qy 653 KTLKSGYTEKQRDRFLSEASIMQFDPHPNVHLEGVVTKSTPVMIITEFMENGLSDSFLR 712
 Db 671 KTLKSGYTEKQRDRFLSEASIMQFDPHPNVHLEGVVTKSTPVMIITEFMENGLSDSFLR 730
 Qy 713 QNDGQFTVIQLVGMLRGIAAGMKYLDAMNVVHRLDLAARNILVNSNLVCKVSDFGSLRPLE 772
 Db 731 QNDGQFTVIQLVGMLRGIAAGMKYLDAMNVVHRLDLAARNILVNSNLVCKVSDFGSLRPLE 790
 Qy 773 DDTSDPTYSALGKGIPIRWTAPEAQYRKFTSADSVMSYGIVMWEVMSYGERPYDWMTN 832
 Db 791 DDTSDPTYSALGKGIPIRWTAPEAQYRKFTSADSVMSYGIVMWEVMSYGERPYDWMTN 850
 Qy 833 QDVINAIEQDYRLPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWRNPNSLKA 892
 Db 851 QDVINAIEQDYRLPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWRNPNSLKA 910
 Qy 893 MAPLSSGINPLLDRTIPDYTSFNTVDWEWLEAIKMGQYKESFANAGTSTFDVYSQMMED 952
 Db 952 MAPLSSGINPLLDRTIPDYTSFNTVDWEWLEAIKMGQYKESFANAGTSTFDVYSQMMED 952


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Db 911 MAPLSSGNPLLDRTIPDYTSFNTVDWLDAIKMSQKESFASAGTFTFDIVSQMTVED 970
Qy 953 ILRLGVTLAGHOKKILNSIQWMRAQMNQIOSVEV 986
Db 971 ILRLGVTLAGHOKKILNSIQWMRAQMNQIOSVEV 1004

RESULT 7
EPB2_COTJA
ID_EPB2_COTJA STANDARD; PRT; 987 AA.
AC Q90344;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
  kinase receptor QEK5).
GN Name=EPHB2; Synonyms=QEK5;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=9610931; PubMed=8612986;
RA Kenny D., Bronner-Frazer M., Marcelle C.;
RT "the receptor tyrosine kinase QEK5 mRNA is expressed in a gradient
  within the neural retina and the tectum.";
RL Dev. Biol. 172:708-716(1995).
CC -!- FUNCTION: Receptor for members of the ephrin-B family.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
  tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the tyr family of protein kinases. Ephrin
  receptor subfamily.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/
  or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X91737; CAA62862.1; -.
CC HSSP; P54763; 1JPA.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR001090; Ephrin receptor.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR003961; FNIII.
CC InterPro; IPR008979; FN III-like.
CC InterPro; IPR008979; Gal bind like.
CC InterPro; IPR001009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001660; SAM_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC InterPro; IPR001426; Ykase_receptorV.
CC Pfam; PF01404; Ephrin_lbd; 1.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00536; SAM; 1.
CC PRINTS; PR00014; FNYPEIII.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00615; EPH_lbd; 1.
CC SMART; SM00060; FN3_2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TyrcK; 1.
CC
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DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
DR PROSITE; PS00853; FN3_2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; FALSE NEG.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 987 Ephrin type-B receptor 2.
FT DOMAIN 20 544 Extracellular (Potential).
FT TRANSMEM 545 565 Potential.
FT DOMAIN 566 987 Cytoplasmic (Potential).
FT DOMAIN 185 322 Cys-rich.
FT DOMAIN 427 427 Fibronectin type-III 1.
FT DOMAIN 433 528 Fibronectin type-III 2.
FT DOMAIN 622 885 Protein kinase.
FT DOMAIN 914 978 SAM.
FT SITE 985 987 PDZ-binding motif (Potential).
FT NP_BIND 628 636 ATP (By similarity).
FT BINDING 654 654 ATP (By similarity).
FT ACT_SITE 747 747 Phosphotyrosine (by autocatalysis)
FT MOD_RES 597 597 (Potential).
FT MOD_RES 603 603 Phosphotyrosine (by autocatalysis)
FT MOD_RES 781 781 (Potential).
FT MOD_RES 931 931 Phosphotyrosine (by autocatalysis)
FT CARBOHYD 266 266 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 337 337 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 429 429 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 478 478 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 483 483 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 987 AA; 110331 MW; 05D6EC68E718DD7 CRC64;

Query Match 95.3%; Score 4945; DB 1; Length 987;
Best Local Similarity 94.9%; Pred. No. 1.7e-300; Indels 0; Gaps 0;
Matches 927; Conservative 30; Mismatches 20;

Qy 10 LLLPLLLAAVEETLMDSTTATAEFGWVHPSPSGEVSVDENNMNTIRTYQVCNPFESSQ 69
Db 11 LALLPLLLAAVEETLMDSTTATAEFGWVHPSPSGEVSVDENNMNTIRTYQVCNPFESSQ 70
Qy 70 NNWLRTKPIRRRGARHRIHVEMKESVDCCSIPSPGSKETFNLYYYEADFDSATKTFPN 129
Db 71 NNWLRTKPIRRRGARHRIHVEMKESVDRDCSSIPNVPGSKETFNLYYYESDFDSATKTFPN 130
Qy 130 WMENPWVKVDITAADESFQVDLGGVWVKINTVRSFGVPVRSRGFYLAFOYGGCMSLIA 189
Db 131 WMENPWVKVDITAADESFQVDLGGVWVKINTVRSFGVPVRSRGFYLAFOYGGCMSLIA 190
Qy 190 VRVYFKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
Db 191 VRVYFKCPRIIQNGADFQETLSGAESTSLVASRGTCINKAEVDVPIKQHCNGDGEWLV 250
Qy 250 PIGRCMKAGFAVENGTVCRCGCSGTFFKANGDEACTHCPINSTRTSEGATNCVCRNGY 309
Db 251 PIGRCMCRPGYESVANGTVCRCGCSGTFFKASQSGDEGCVHCFINSTRTSEGATNCVCRNGY 310
Qy 310 YRADLDPDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369
Db 311 YRADADPVDMPCTTIPSAQSVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 370
Qy 370 GACTRCGDNVQVAPROGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQASVNI 429
Db 371 GACTRCGDNVQVAPROGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQASVNI 430
Qy 430 TTNQAAPSAYSIMHOVSRTVDSITLWSQDQPNGLVDYELQYKEKELSEYNATAIKSP 489
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Db 431 TTNQAPSAVSIMHQVSRVDSITLSWSQDPQNGVILDYELQYKKNLSSELNSTAVKSP 490
Qy 490 TINTVVOGLKAGAIYVFQVARTVAGYGRYSGKMYFQMTTEAEYQTSIQEKLPLIGSSA 549
Db 491 TINTVVOQLKAGTIYVFQVARTVAGYGRYSGKMYFQMTTEAEYQTSIQEKLPLIGSSA 550
Qy 550 AGLVFLAVVIAVNCNRGPERADSEYTDKLOHYTSGHMTGPKKIYIDPFTYEDPNEAV 609
Db 551 AGLVFLAVVIAVNCNRGPERADSEYTDKLOHYTSGHMTGPKKIYIDPFTYEDPNEAV 610
Qy 610 REPAKEIDISCVKTEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGVTEKORRDFLS 669
Db 611 REPAKEIDISCVKTEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGVTEKORRDFLS 670
Qy 670 EASIMGQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQVGLMLRG 729
Db 671 EASIMGQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQVGLMLRG 730
Qy 730 IAAGMKYLAADNYYVHRLAARNILVNSNLVKCVSDPGLSRPLEDDTSDPTTYSALGKIP 789
Db 731 IAAGMKYLAADNYYVHRLAARNILVNSNLVKCVSDPGLSRPLEDDTSDPTTYSALGKIP 790
Qy 790 IRWTAPAIQYRKFTSADVMSYGVIVMVEVMSYGERPYVDMTNDQVINAIEQDYRLPPLPM 849
Db 791 IRWTAPAIQYRKFTSADVMSYGVIVMVEVMSYGERPYVDMTNDQVINAIEQDYRLPPLPM 850
Qy 850 DCPSALHQLMDCQKQDRNHRPKFGQIVNTLDMKMRNPNSLKAWAPLSSGINPLFLDRTI 909
Db 851 DCPNALHQLMDCQKQDRNHRPKFGQIVNTLDMKMRNPNSLKAWAPLSSGINPLFLDRTI 910
Qy 910 PDYTSFNTVDEWLBAIKMGQYKESFANAGTSPFVVSQMMEDILRLGVTLAGHOKKILN 969
Db 911 PDYTSFNTVDEWLBAIKMGQYKESFANAGTSPFVVSQMMEDILRLGVTLAGHOKKILN 970
Qy 970 SIQVRAQMNQIQSVEV 986
Db 971 SIQVRAQMNQIQSVEV 987

RESULT 8
EPB1 RAT
ID EPB1 RAT STANDARD; PRT; 984 AA.
AC P09759;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein
kinase receptor Eph-2) (ELK).
GN Name=Ephb1; Synonyms=Eph2, Elk;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=91203869; PubMed=2017163;
RA Lhotak V., Greer P., Letwin K., Pawson T.;
RT "Characterization of elk, a brain-specific receptor tyrosine kinase.";
RL Mol. Cell. Biol. 11:2496-2502(1991).
RN [2]
RN SEQUENCE OF 605-984 FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=94167102; PubMed=2485255;
RA Letwin K., Yee S.P., Pawson T.;
RT "Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned
using anti-phosphotyrosine antibody.";
RL Oncogene 3:621-627(1988).
CC -1- FUNCTION: Receptor for members of the ephrin-B family. Binds to
ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions
in the nervous system.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.

CC -1- SUBUNIT: The ligand-activated form interacts with GRB2, GRB10 and
NCK through their respective SH2 domains. The GRB10 SH2 domain
binds EphB1 through Tyr-928, while GRB2 binds residues within the
catalytic domain. The NCK SH2 domain binds EphB1 through Tyr-594.
CC Interacts with PRKABP (By similarity).
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Restricted to brain and testes.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M59814; -; NOT ANNOTATED_CDS.
CC EMBL; X13411; CA31777.1; -;
CC PIR; A39753; A39753.
CC HSP; P54763; J3PA.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR001090; Ephrin_receptor.
CC InterPro; IPR003962; FniIII subd.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR008979; Gal_bind-like.
CC InterPro; IPR011009; Kinase-like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001660; SAM.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC InterPro; IPR001426; Ykase_receptorV.
CC Pfam; PF01404; Ephrin_lbd; 1.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00536; SAM; 1.
CC PRINTS; PR00014; FNTYPEIII.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00615; EPH_lbd; 1.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TYRK; 1.
CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC PROSITE; PS50105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 984 Ephrin type-B receptor 1.
FT DOMAIN 18 540 Extracellular (Potential).
FT TRANSMEM 541 563 Potential.
FT DOMAIN 564 984 Cytoplasmic (Potential).
FT DOMAIN 183 319 Cys-rich.
FT DOMAIN 323 424 Fibronectin type-III 1.
FT DOMAIN 430 525 Fibronectin type-III 2.
FT DOMAIN 619 882 Protein kinase.
FT DOMAIN 911 975 SAM.
FT SITE 982 984 PDZ-binding motif (Potential).
FT NP_BIND 625 633 ATP (By similarity).
FT BINDING 651 651 ATP (By similarity).
FT ACT_SITE 744 744 By similarity.
FT MOD_RES 594 594 Phosphotyrosine (by autocatalysis)

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FT MOD_RES 600 600 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT MOD_RES 778 778 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT MOD_RES 928 928 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 426 426 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 984 AA; 109882 MW; 521EAC240D8F91A CRC64;

Query Match
Best Local Similarity 75.8%; Score 3934.5; DB 1; Length 984;
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;

QY 11 LLLPLLAETLMDSTATAELGMVHPHSGWEEVSGYDENWNTIRTYQVCNVFSSQN 70
D 11 LLLPLLAETLMDSTATAELGMVHPHSGWEEVSGYDENWNTIRTYQVCNVFSSQN 69
QY 71 NWLRTKFIIRRGARRIHVENKFSVRDCSSITPSVSGCKETFNLYYYEADFSATKTFPNW 130
D 71 NWLRTKFIIRRGARRIHVENKFSVRDCSSITPSVSGCKETFNLYYYEADFSATKTFPNW 129
QY 131 MENPFWKVDITAADESPQVDLGRVMKINTEVRSFGPVSRSGFYLAFOYGGCMSLIIV 190
D 131 MENPFWKVDITAADESPQVDLGRVMKINTEVRSFGPVSRSGFYLAFOYGGCMSLIIV 189
QY 191 RVFYKPCRIIQAIGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGLWLP 250
D 191 RVFYKPCRIIQAIGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGLWLP 249
QY 251 IGRMCKAGFAENVGVTCGCGSPGTFKANOGBEACHCPINSTRITSEGNATNCVCRNGY 310
D 251 IGRMCKAGFAENVGVTCGCGSPGTFKANOGBEACHCPINSTRITSEGNATNCVCRNGY 308
QY 311 RADLDPLDMPCTTIPSAPOAVISVNETSLMLEWTPDRDSCGREDLVNIIKSCSGSRG 370
D 311 RADLDPLDMPCTTIPSAPOAVISVNETSLMLEWTPDRDSCGREDLVNIIKSCSGSRG 368
QY 371 ACTRCGDNVOYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTQSPSPFASVNIIT 430
D 371 ACTRCGDNVOYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTQSPSPFASVNIIT 428
QY 431 TNQAAPSAVSIHQVSTVDISITLSWOPDQNGVLDVLOYEYKELSEYNATATKSP 490
D 431 TNQAAPSAVSIHQVSTVDISITLSWOPDQNGVLDVLOYEYKELSEYNATATKSP 488
QY 491 NTVTVQGLKAGAIYVFOVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSAA 550
D 491 NTVTVQGLKAGAIYVFOVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSAA 548
QY 551 GLVPLIAVVAIVCNRRGFERADSEYTDKLOHYTSGHMTGPKMKIYIDPTTYEDPNEVR 610
D 551 GLVPLIAVVAIVCNRRGFERADSEYTDKLOHYTSGHMTGPKMKIYIDPTTYEDPNEVR 608
QY 611 EFAKEIDISCVKLEOVIGAGEFGVCSGHLKLPKREIFVAIKLKSQYTEKORRDPFSE 670
D 611 EFAKEIDISCVKLEOVIGAGEFGVCSGHLKLPKREIFVAIKLKSQYTEKORRDPFSE 668
QY 671 ASIMGQFDHPNVHLEGVVTWKTVMIIITBFMENGSLDSFLRQNDGQFTVIQVGLMRLGI 730
D 671 ASIMGQFDHPNVHLEGVVTWKTVMIIITBFMENGSLDSFLRQNDGQFTVIQVGLMRLGI 728
QY 731 AAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTTYSALGGKIP 790
D 731 AAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTTYSALGGKIP 788
QY 791 RWTAPAEIQRKFTSASDVMSYGIWMEVMSYGERPYWMDTNDQVINAISQDYLRLPPMD 850
D 791 RWTAPAEIQRKFTSASDVMSYGIWMEVMSYGERPYWMDTNDQVINAISQDYLRLPPMD 848
QY 851 CPSALHQLMLDCWQKDRNRPKFGQIVNTLDKMIKIRNPNSLKAMAPLSSGINLPILDR 910
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Db 849 CPAALHQLMLDCWQKDRNRPKFAEIVNTLDKMIKIRNPASIKTKVATITAVPSQPLDRSIP 908
QY 911 DYTSTFVTVDEWLEAKMGQYKESFANAGTSDVVSQMMEDILRLGVTLGAGHOKILNS 970
Db 909 DETAFTVDDWLSAIKMWQYRDSFLTAGFTSLQVLTQMTSDLLRIGVTLGAGHOKILNS 968
QY 971 IQVMRAQMNQIOQSV 984
Db 969 IHSMRVQMNQSPSV 982

RESULT 9
Q8CBF3 PRELIMINARY: PRT; 984 AA.
AC Q8CBF3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630041E07 product:Eph receptor B1, full
DE insert sequence.
GN Name=EphA1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=96115594; PubMed=8666391;
 RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,
 RA Pleasure D.E., Ikegaki N.;
 RT "cDNA cloning, molecular characterization, and chromosomal
 RT localization of NET(EPH2), a human EPH-related receptor protein-
 RT tyrosine kinase gene preferentially expressed in brain.";
 RL Genomics 29:426-437(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RC TISSUE=Kidney;
 RA Stein E., Schoecklmann H.O., Daniel T.O.;
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 18-32.
 RA Zhang Z., Henzel W.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Submitted (JUN-2004) to Swiss-Prot.
 RN [4]
 RP INTERACTIONS WITH GRB2 AND GRB10.
 RX MEDLINE=96394464; PubMed=8798570;
 RA Stein E., Cerretti D.P., Daniel T.O.;
 RT "Ligand activation of ELK receptor tyrosine kinase promotes its
 RT association with Grb10 and Grb2 in vascular endothelial cells.";
 RL J. Biol. Chem. 271:23588-23593(1996).
 CC [1]- FUNCTION: Receptor for members of the ephrin-B family. Binds to
 CC ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions
 CC in the nervous system.
 CC [2]- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC [3]- SUBUNIT: The ligand-activated form interacts with GRB2, GRB10 and
 CC NCK through their respective SH2 domains. The GRB10 SH2 domain
 CC binds EPHB1 through Tyr-928, while GRB2 binds residues within the
 CC catalytic domain. The NCK SH2 domain binds EPHB1 through Tyr-594.
 CC Interacts with PRKCAP (By similarity).
 CC [4]- SUBCELLULAR LOCATION: Type I membrane protein.
 CC [5]- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=EPHB1A;
 CC IsoId=P54762-1; Sequence=Displayed;
 CC Name=2; Synonyms=EPHB1B;
 CC IsoId=P54762-2; Sequence=VSP_003013;
 CC Name=3; Synonyms=EPHB1C;
 CC IsoId=P54762-3; Sequence=VSP_003015;
 CC Name=4; Synonyms=EPHB1D;
 CC IsoId=P54762-4; Sequence=VSP_003014;
 CC [6]- TISSUE SPECIFICITY: Preferentially expressed in brain.
 CC [7]- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 CC [8]- SIMILARITY: Contains 2 fibronectin type III domains.
 CC [9]- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L40636; AAB08520.1; -;
 CC EMBL; AF037331; AAD02030.1; -;
 CC EMBL; AF037332; AAD02031.1; -;
 CC EMBL; AF037333; AAB94627.1; -;
 CC EMBL; AF037334; AAB94628.1; -;
 CC HSSP; P54763; 1JPA.
 CC InAct; P54762; -;

DR Genew; HGNC:3392; EPHB1.
 DR MIM; 60600; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; YKase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00699; Pkinase; 1.
 DR PRINTS; PR00014; ENTYPRIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyTKC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Direct protein sequencing;
 KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 17
 FT CHAIN 18 984 Ephrin type-B receptor 1.
 FT DOMAIN 18 540 Extracellular (Potential).
 FT TRANSMEM 541 563 Potential.
 FT DOMAIN 564 984 Cytoplasmic.
 FT DOMAIN 183 319 Cys-rich.
 FT DOMAIN 323 424 Fibronectin type-III 1.
 FT DOMAIN 430 525 Fibronectin type-III 2.
 FT DOMAIN 619 882 Protein kinase.
 FT DOMAIN 911 975 SAM.
 FT SITE 982 984 PDZ-binding motif (Potential).
 FT NP_BIND 625 633 ATP (By similarity).
 FT BINDING 651 651 ATP (By similarity).
 FT ACT_SITE 744 744 By similarity.
 FT MOD_RES 594 594 Phosphotyrosine (by autocatalysis).
 FT MOD_RES 600 600 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 778 778 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 928 928 Phosphotyrosine (by autocatalysis).
 FT CARBOHYD 334 334 N-linked (GlcNAc..) (Potential).
 FT CARBOHYD 426 426 N-linked (GlcNAc..) (Potential).
 FT CARBOHYD 480 480 N-linked (GlcNAc..) (Potential).
 FT VARSPPLIC 1 27 MALDYLLLLLAAGAAVAMEETLMDTTRT -> METREKKKGR
 FT AERGTR (in isoform 2).
 FT FTID=VSP_003013.
 FT Missing (in isoform 4).
 FT FTID=VSP_003014.
 FT Missing (in isoform 3).
 FT FTID=VSP_003015.
 FT T -> S (in dbSNP:1042794).
 FT FTID=VAR_011801.

[illegible]


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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057301; AAH57301.1; -.
KW Receptor.
SQ SEQUENCE 984 AA; 109924 MW; 2E2F89942A8041A9 CRC64;

Query Match 75.5%; Score 3916.5; DB 2; Length 984;
Best Local Similarity 73.7%; Pred. No. 3.7e-236;
Matches 718; Conservative 127; Mismatches 128; Indels 1; Gaps 1;

QY 11 LLLPLAAVEETLMDSTTATLGLGHWVPPSGWEVSGYDENMANTIRYQVNCVPESSON 70
DB 10 LLASAAVEETLMDTRTATLGLGHWVPPSGWEVSGYDENMANTIRYQVNCVPESSON 69
QY 71 NWLRTKFRRRGAIRIHVEMKFSVRDCSSIPVSGSKCTETNLYYEAADPSATKTFPNW 130
DB 70 NWLLTTFINRRGAIRIYTEMFTVRDCSSLPNVPGSKCTETNLYYETSDVIATKSAFW 129
QY 131 MENPMVKYDTTAADESPQVDLGGVRMKINTEVRSFGVSRSGFYLAQDYGCGMSLIAV 190
DB 130 SEAPYLKVDTTAADESPQVDLGGVRMKINTEVRSFGVSRSGFYLAQDYGCGMSLLSV 189
QY 191 RVFRKCPRIITONGAIPOETLSGABSTSLVAARSGCIANABEVDPVILKYNCGDEMLVP 250
DB 190 RVFFIKCPISIVQNEFAVPTTGTAEESTSLVIARTGTCIPNABEVDVPIKLYCNGDGEWVP 249
QY 251 IGRWCCKAGFAVGTGRCPCGCTKCANOGDEACTHCPINSTRTSEGATNCVCRNGY 310
DB 250 IGRCTCKGYP-ENSVACKACPACTFKASQAEAGCHCPSNSRSPSEAPICRTGY 308
QY 311 RADLDPLDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSCGREDLVNIIICKSGSGRG 370
DB 309 RADFPPEVACTSPVSGPRNIVISVNETSIILEWHPPRETGTRDDVYNIICKCRADR 368
QY 371 ACTRCGNVQVAPQLGLTEPRIVISDLAHTQYTFEIQVNGVTDGSPSPQFASVNIT 430
DB 369 SCSCDDNVFVPRQLGLTECRVSISSLWHTPTFTDQAINGVSSKSPFPQHVSNIT 428
QY 431 TNOAPSAVSIHVOVSRVDSITLSWQDOPGVNLDYQYKELSEYNATAIKSPT 490
DB 429 TNOAPSTVPIHQVSAVTRISITLSWQDOPGVNLDYQYKELSEYNATAIKSPT 488
QY 491 NTVTVQGLKAGAIYVQVARTVAGYGRYSKGMFTQMTAEAYQTSIQEKLPLIGSSAA 550
DB 489 NTARIDGLRPGWVYVQVARTVAGYGRYSKGMFTQMTAEAYQTSIQEKLPLIGSSAA 548
QY 551 GLVFLIAVVVTAICNRRGFRADSEYTDKLOHTSGHMTGMIYIDPFTYEDPNEAVR 610
DB 549 GWVFWSLVAISIVCSRKRAYSKEAAYSQKLYHSTGRSGPMKIYIDPFTYEDPNEAVR 608
QY 611 EFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRREIFVAIKTLKSGYTEKQRDFLSE 670
DB 609 EFAKEIDVSFKIEVIGAGFEGVGRKLPGRREIYVAIKTLKAGYSKQRDFLSE 668
QY 671 ASIMGQDHPNVIHLEGVTKSTPMIITEFWENGSLDSFLRQNDGQFTVQLVGLMRLGI 730
DB 669 ASIMGQDHPNRIIRLEGVTKSRPVMIIITEFWENGALDSFLRQNDGQFTVQLVGLMRLGI 728
QY 731 AAGMKYLAQVYVHRDLAARNILNSNLVCKVDFGLSRFLSDTSDPTYSALGGKIP 790
DB 729 AAGMKYLAQVYVHRDLAARNILNSNLVCKVDFGLSRFLSDTSDPTYSALGGKIP 788
QY 791 RWTAPALQVKEFTSASDVNSYGVIMVMSYGERPYWDMNQVINAIEDYELPPMD 850
DB 789 RWTAPALQVKEFTSASDVNSYGVIMVMSYGERPYWDMNQVINAIEDYELPPMD 848
QY 851 CPSALHQLMDCWQKDRNRHFKFGQIVNTLDKMRNPNSLKAMAPLSGGINLPDLRTIP 910
DB 849 CPAALHQLMDCWQKDRNRHFKFGQIVNTLDKMRNPNSLKATVATITAVSQPLDRLSIP 908
QY 911 DYTSTNTVDEWLEAIKMGQYKESFANAGTSTFVVSQMMEDILRLGVTLAGHOKKILNS 970
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DR Pfam: PF00536; SAM; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyrcKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FALSE_NEG.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00105; SAM DOMAIN; 1.
DR ATP-binding; Glycoprotein; Receptor; Repeat; Signal;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 19
FT CHAIN 20 985
FT DOMAIN 20 542
FT TRANSMEM 543 563
FT DOMAIN 564 985
FT DOMAIN 185 321
FT DOMAIN 325 426
FT DOMAIN 436 527
FT DOMAIN 620 883
FT DOMAIN 912 976
FT SITE 983 985
FT NP_BIND 626 634
FT BINDING 652 652
FT ACT_SITE 745 745
FT MOD_RES 595 595
FT MOD_RES 601 601
FT MOD_RES 779 779
FT MOD_RES 929 929
FT CARBOHYD 336 336
FT CARBOHYD 428 428
FT CARBOHYD 482 482
FT SEQUENCE 985 AA; 110104 MW; BE72CD1BFF51E623 CRC64;

Query Match 72.6%; Score 3767; DB 1; Length 985;
Best Local Similarity 71.2%; Pred. No. 8.2e-227;
Matches 699; Conservative 131; Mismatches 140; Indels 12; Gaps 5;

QY 6 LGALLLLPL---LAAVEETLMDSTTATBELGMMVPPSGWEVSGYDENMNTIRYQV 61
DB 3 LNVLLLLCLSGGQGVAVEETLMDTRTATBELGTANPSSGWEVSGYDENLNTIRYQV 62
QY 62 CNVFESSQNNWLRTKTRRRGAHRHIVEMKFSVRDCSIPSPGCKETFNLYYYEADF 121
DB 63 CNVFGPKQNNLLTTFIPRGAHRVYVEMRTVRDCSLPNVPGCKETFNLYYYEADS 122
QY 122 SATKTFPNMENPWNKVDITIAADEFSQVDLGGVRMKNINTEVRSGVSRGFFLAFQDY 181
DB 123 IENKISTFWNESPVLKVDITIAADEFSQVDGGLMKVNTVEVRSFGPLTRSGFFLAFQDY 182
QY 182 GGCNLSIAVRVYRCPRIQNGAIFQBTLSGAESTSLVAARGSCIANAEVDVPIKLYC 241
DB 183 GACNLSLSVRVFFKEMPSPVQNLVFPETMTGAESTSLVIARGTCIPNAEVDVPIKLYC 242
QY 242 NGDEWLVPICRCMKAGFEAVENGTCVRCGSPGTFKANOQDEACTHCPCINSRTSEGAT 301
DB 243 NGDGEWVPIGKCTCKAGYEP-ENHVVCACPAAMFKANQGMGICACQFANSRSTSEASP 301
QY 302 NCVCNGYVRADLDPLDMPCTIPSPAPQAVLSSVNETSLMLEWTPPRDSGGREDLVNII 361
DB 302 ICICRNGYVRADFDTPPEAPCTSPVSGPRNVISIVNETAITLEWHPPRETGGRDVDYIV 361

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RESULT 14

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O57458 PRELIMINARY; PRT; 815 AA.
AC O57458;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EphB2-tyrosine kinase receptor (Fragment).
GN Name=xEPH2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99008330; PubMed=9794228;
RA Tanaka M., Wang D.Y., Kamo T., Igarashi H., Xiang Y.Y.,
RA Tanioka F., Naico Y., Sugimura H.;
FT "Interaction of EphB2-tyrosine kinase receptor and its ligand conveys
RT dorsalization signal in Xenopus laevis development.";
RL Oncogene 17:1509-1516(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
DB EMBL; AF026039; AAB94603.1; -.

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QY 362 CKSGSGRACGTRCGDNVOYAPRQLGLTEPRIVISDLAHTQVTFEIOAVNGVTDSPFS 421
DB 362 CKKCRADRRACSCDDNDVDFPRQLGLTTRVFISNLMAHTPTTFETQAVNGVTKSPFP 421
QY 422 POPASVNIITNQAAAPSASVIMHQVSTVDSITLWSQDPQPNQVILDYLOYYEKLSY 481
DB 422 PQHVSVNIITNQAAAPSSVPMHQVKATMKSITLSWFOEQPNQGIILDYIRYEEKDHF 481
QY 482 NATAIKSPNTVTVOGLKAGAIYVF---OVRARTVAGYGRYSGMYFOFMTAEAYOTSIQ 538
DB 482 NSSLARQNTARTG---GRVVMFMSVQVARTVAGYGRKFSKCGFQILTAEYKSEIR 538
QY 539 EKPLLIIGSSAAGLVFLIAVVIACVNRGRFERADSEYTKLOHYTSGHMTPGMKIYID 598
DB 539 EQPLP-TGSAAGVFIIVSLVAISIVCSRKRTYSKEAVYSDKLQHYSTGRSGPMKIYID 597
QY 599 PFTYEDPNEAVRFAKEIDISCVKIEQVIGAGFGEVCSGHKLKPKREIFVAIKTLKSG 658
DB 598 PFTYEDPNEAVRFAKEIDISFVKIEBIGAGFGEVYGRKLKPKREISVAIKTLKAG 657
QY 659 YTEKQRDDFLSEASIMGQFDHPNVHLEGVWTKSTPWIITEPMENGSLDSPLRQNDGOF 718
DB 658 YSEKQRDDFLSEASIMGQFDHPNIIIRLEGVWTKSRPWIITEPMENGALDSFLRQNDGOF 717
QY 719 TVIQLVGLRGIAAGMKYLADNMVYHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDP 778
DB 718 TVIQLVGLRGIAAGMKYLSENNYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDP 777
QY 779 TYSALGGKIPINWTAPEALQHRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINA 838
DB 778 TYSALGGKIPINWTAPEALQHRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINA 837
QY 839 IEQDYRLPPMDPCPSALHOLMDCWQKDRNHRKFGQIVNTLDMIRNPNLSKAMAPLSS 898
DB 838 IEQDYRLPPMDPCPSALHOLMDCWQKDRNHRKFGQIVNTLDMIRNPNLSKAMAPLSS 897
QY 899 GINPLDLDRTPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDIIRLGV 958
DB 898 VPSQPLDLDRTPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDIIRLGV 957
QY 959 TLAGHOKKILNSIQVMRAQMNQ 980
DB 958 TLAGHOKKILNSIQVMRAQMNQ 979

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DR HSP; P54763; LUPA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0005003; F:ephrin receptor activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FNIII.
DR InterPro; IPR008957; FNIII-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR010993; SAM_homology.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase AS.
DR InterPro; IPR001426; Ykase receptorv.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM_1; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00853; FN3_2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT NON TER 1
SQ SEQUENCE 815 AA; 90848 MW; D36D77C498097BFE CRC64;

Query Match 72.38; Score 3753.5; DB 2; Length 815;
Best Local Similarity 87.18; Pred. No. 4.4e-226;
Matches 710; Conservative 49; Mismatches 55; Indels 1; Gaps 1;

QY 173 GFYLAFOYGGCSLIAVRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAE 232
DB 1 GFYLAFOYGGCSLIAVRVYDRKCPRIIQNGAIFQETLSGAESTSLVAARGCMPNAEE 60
QY 233 VDVPILKYNCGDGBWLVPICRMCAGFAVENGTVCRCGSPGPFKANKQGDCACTHCPIN 292
DB 61 VDVPILKYNCGDGBWLVPICRCLCAGYSEVNGTCRDVPVGMFKANKQGDSDSLHCPIN 120
QY 293 SRTTSEGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMELWTPPRDSGG 352
DB 121 SRTTSEGATNCVCRNGYRSDSLHQMCHCTTIPSAQONVSSVKQTSMLLEXAPPRDSGG 180
QY 353 REDLVYNIICKSCSGRGACTRCGDNVQVAPROLGLTEPRIYISDLAHTQYTFEIOAVN 412
DB 181 REDLVYHIICKSCSGRGAYTHCGDNVQAPAPQGLMEPRVYMSDLAHTQYTFEIOAVN 240
QY 413 GVTDSQSPFQFASVNTTNOAAPSAYSIMHQSRTVDSITLSQSPQDPNGVILDYELQ 472
DB 241 GVTDSQSPFHSVNTTNOAAPSAYSIMHLVTRADISITLSQSPQDPNGIILDYELL 300
QY 473 YYEKELSEYNATAIKSTNTVTVOGLKAGALYVQVARTVAGRYSGMYQFTWTEAE 532
DB 301 YDEKDLTEHNSRQSQSTNTVLVPLRAGTIYFQVLRRMAGRYSGMYQFTWTEAE 360

533 YQTSIQEKLPLIIIGSSAAGLVFLIAVVIIVCN-RRGFERADSEYTDKLOHYTSGHMT 591
DB 361 YQSSFQEKPLIIIGSSAAGLVFLIALVIIIVCSRRRGERADYEYTDKLOHYTSGHMT 420
QY 592 GMKIYIDPFYEDPNEAVREFAKEIDISCVKIBQVIGAGEGVCSEHKLKLPGRREIFVA 651
DB 421 GMKIYIDPFYEDPNEAVREFAKEIDISCVKIBQVIGAGEGVCSEHKLKLPXXREIFVA 480
QY 652 IKTLKSGYTEKQRDRFLSEASIMQGFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFL 711
DB 481 IKTLKSGYTEKQRDRFLSEASIMQGFDPNVIHLEGVVTKSSPVMIIITEFMENGLSDSFL 540
QY 712 RQNDGQFTVIQLVGLMRLGIAAGMKYLADMYVVRDLAARNILVNSNLVCKVDSFGLSRFL 771
DB 541 RQNDGQFTVIQLVSMRLGIAAGMKYLANMYVVRDLAXXNLLVNSNLVCKVDSFGLSRFL 600
QY 772 EDDTSPTYSALGGKIPRTWTAPEALQYRKFTSASDVNSYGIWMVEVMSYGERPYWMT 831
DB 601 EDDTSPTYSALGGKIPRTWTAPEALQYRKFTSASDVNSYGIWMVEVMSYGERPYWMT 660
QY 832 NQDVINAIEQDYRLPPMDPCPSALHOLMDCWOKDRNRPKFGQIVNTLDKMIKRNPSLK 891
DB 661 NQSAIHAIVQDYRLPPMDPCFNALHQLLLDCWQKDRNRPKFGQIVNTLDKMIKRNPTIK 720
QY 892 AMAPLSSGINLPLDRTIPDYSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQWME 951
DB 721 AVAPLSSGVTPLDRLTPAYTSLSRGDEWLDALKMAQYKESFANAGFTSFDVVSQWME 780
QY 952 DIILRGVTLAGHOKKILNSIQVWRAQMNQIQSVEV 986
DB 781 DIILRGVTLAGHOKKILNSIQVWRAQMNQIQSVEV 815

RESULT 15
EPBL_CHICK
ID EPBL_CHICK STANDARD; PRT; 984 AA.
AC Q07494;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 1 (EC 2.7.1.112) (Tyrosine-protein kinase
DE receptor EPH-2) (Tyrosine kinase CEK6 receptor) (fragment).
GN Names=EPHBI; Synonyms=CEK6;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Fasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -I- FUNCTION: Receptor for members of the ephrin-B family. Binds to
CC ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions
CC in the nervous system.
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed at high levels in the 10-day embryo,
CC and in adult brain, lung, heart and skeletal muscle. Low levels of
CC expression detected in all other adult tissues tested.
CC -I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC -I- SIMILARITY: Contains 2 fibronectin type III domains.
CC -I- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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 ENBL; Z19110; CAA79526.1; -;
 HSP; P54763; 1JPA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; Ephrin_subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase AS.
 DR InterPro; IPR001426; V_kase receptor.
 DR Pfam; PF01404; Ephrin_lbd_1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50853; FN3_2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; PARTIAL.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 FT NON_TER 1
 FT DOMAIN <1 541 Extracellular (Potential).
 FT TRANSMEM 542 562 Potential.
 FT DOMAIN 563 984 Cytoplasmic (Potential).
 FT DOMAIN 164 300 Cys-rich.
 FT DOMAIN 304 405 Fibronectin type-III 1.
 FT DOMAIN 411 525 Fibronectin type-III 2.
 FT DOMAIN 619 882 Protein kinase.
 FT DOMAIN 911 975 SAM.
 FT SITE 982 984 PDZ-binding motif (Potential).
 FT NP_BIND 625 633 ATP (By similarity).
 FT BINDING 651 651 ATP (By similarity).
 FT ACT_SITE 744 744 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 594 594 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 600 600 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 778 778 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 928 928 Phosphotyrosine (by autocatalysis) (Potential).
 SQ SEQUENCE 984 AA; 109519 MW; EF06C83BB63A13A1 CRC64;

Query Match 71.7%; Score 3721; DB 1; Length 984;
 Best Local Similarity 70.3%; Pred. No. 6.2e-224;
 Matches 688; Conservative 121; Mismatches 150; Indels 20; Gaps 2;
 21 ETLMDSITATAEALGVHPPSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKEIRR 80
 1 ETLMDSITATAEALGVHPPSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKEIRR 60
 81 RGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYETDVIATKSAFWTEAPYLKVDVT 140

Db 61 RGAHRIYTEMRTFVRDCSSIPSPGCKETFNLYYETDVIATKSAFWTEAPYLKVDVT 120
 Qy 141 IAADESFSQVDLGGCRVWKINTEVRSFGPVSRSFGFYLAQDYGGCMLIAVRYFRCPRI 200
 Db 121 IAADESFSQVDFGRLMKGXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFFKCPSP 180
 Qy 201 IONGAIFQETLGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKAGF 260
 Db 181 VQNFALFPETMTGAESTSLVARGTCIPNAEEVDVPIKLYCNGDGEWLVPIGRCMKAGY 240
 Qy 261 EAVENGTVCRGCPSGTFFKANOQDEACTHCPIINSRTTSEGATNCVCRNGYYRADLDP 320
 Db 241 EP-ENNVACRACPAFTFKASQAGLCAACPPNSRSSAEASPLCACRNGYFADLDP 299
 Qy 321 CTTPSAPQAVISSVNETSILEWTPRDSGGEDLVNIIKSCSGSGACACTCCGDNQ 380
 Db 300 CTSVPSGPRNVISIVNETSIIILEWNPRTGGDDVTYIVIVCKKRRARRACRCDNVE 359
 Qy 381 YAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOAAPS 440
 Db 360 FVPRQLGLTETRVFISLWHTPYTFEIOAVNGVSNKSPFPPOHVSNTTNOAAPS 419
 Qy 441 IMHVSATWRSITLSPQEPQNGIILDYELRYEKLRICTPDVSGTVGSRPADHNEY 479
 Db 420 IMHVSATWRSITLSPQEPQNGIILDYELRYEKLRICTPDVSGTVGSRPADHNEY 479
 Qy 482 NATAIKSPNTVTVOGLKAGAIYVFOVARTVAGYSGKMYFOFMTAEYQTSIOEKL 541
 Db 480 NSSVARSQNTARLEGLRFGVMYVQVARTVAGYSGKMYFOFMTAEYQTSIOEKL 539
 Qy 542 PLIGSSAAGLVFLIAVWIAIVCNRRGPERADSEYTDKLQHYTSGHMTGPKMIYDP 601
 Db 540 PLIGSSAAGLVFLIAVWIAIVCNRRGPERADSEYTDKLQHYTSGHMTGPKMIYDP 599
 Qy 602 YEDPNEAVREFAKEIDVSVFKIEBEVIGAGFGEVGVCSGHLKLPKREIFVAIKL 661
 Db 600 YEDPNEAVREFAKEIDVSVFKIEBEVIGAGFGEVGVCSGHLKLPKREIFVAIKL 659
 Qy 662 KQRDFLSEASIMGQFDHNVHLEGVVTKSTPMIITFMENGSLDSFLRQNDGQFTVI 721
 Db 660 KQRDFLSEASIMGQFDHNVHLEGVVTKSTPMIITFMENGSLDSFLRQNDGQFTVI 719
 Qy 722 QLVGLRGIAAGKYLADNMVHRDLAARNILVSNLVCVSDGLSRLEDDTSDPTYT 781
 Db 720 QLVGLRGIAAGKYLADNMVHRDLAARNILVSNLVCVSDGLSRLEDDTSDPTYT 779
 Qy 782 SALGGKIPRTWTAPEAIQVRKFTSASDVWSYGIWMVEVMSYGERPYWDMNQVINA 841
 Db 780 SALGGKIPRTWTAPEAIQVRKFTSASDVWSYGIWMVEVMSYGERPYWDMNQVINA 839
 Qy 842 DYRLPPMDCPSALHQLMDCWQDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 901
 Db 840 DYRLPPMDCPSALHQLMDCWQDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 899
 Qy 902 LPLDRTIPDYSFNTVDENLEAIKQYKESFANAGFTSFDVVSQMMEDILRLGVTLA 961
 Db 900 LPLDRTIPDYSFNTVDENLEAIKQYKESFANAGFTSFDVVSQMMEDILRLGVTLA 959
 Qy 962 GHOKKIINSIQVRAQMNQ 980
 Db 960 GHOKKIINSIQVRAQMNQ 978
 RESULT 16
 Q8CBE2 PRELIMINARY; PRT; 943 AA.
 ID Q8CBE2
 AC Q8CBE2
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:9630045017 product:Eph receptor B1, full

Db	429	TNOAPTPTVIMQVSAITMSITLSWQEPQNGIILDIYRIYKEHNEFSSMARSQT	488	RA	Jones S.J., Marra M.A.;
Qy	491	NTVTVOGLKAGAIYVFOVARTVAGYGRYGRMYFQMTAEAYQTSIQEKLPLIISSAA	550	RT	"Generation and initial analysis of more than 15,000 full-length human
Db	489	NTARIDGLRPGWVYVQVARTVAGYKFGKCMCFQTLTDDDKSELREQLPLIAGSAAA	548	RL	and mouse cDNA sequences.";
Qy	551	GLVPLIAVIAVNCNRRGERADSEYTDKLOHTSGHMTPGMKIYIDPTYEDPNEAVR	610	RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Db	549	GVFWFSLVAISVCSRKAYSKEAAYSDKLOHYSTGR	586	RP	[2]
Qy	611	EPAKEIDISCVKIBQVIGAGFEGVCSGHLKLPKREIFVAIKTLKSGYTEKORRDFLSE	670	RC	SEQUENCE FROM N.A.
Db	587	-----GEFGEVYGRKLQKREIYVAIKTLKAGYSEKORRDFLSE	627	RA	Strausberg R.;
Qy	671	ASIMGQDFHNPVHLEGVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQLVGMLRGI	730	RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
Db	628	ASIMGQDFHNPVHLEGVTKSTPVMIIITFPMENGALDSFLRQNDGQFTVIQLVGMLRGI	687	CC	-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
Qy	731	AAGKYLADNMYVRDILAAARNILVNSLVCKVSDPGLSRLEDDTSDPTVTSALGGKIPV	790	CC	tyrosine phosphate.
Db	688	AAGKYLSEMYVRDILAAARNILVNSLVCKVSDPGLSRLEDDTSDPTVTSALGGKIPV	747	CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
Qy	791	RWTAPEAIQYRKFTSASDVMSYGIWVMEVMSYGRPYWDMTQDVINAIEQDYRLPPMD	850	CC	-I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
Db	748	RWTAPEAIYKFTSASDVMSYGIWVMEVMSYGRPYWDMTQDVINAIEQDYRLPPMD	807	CC	receptor subfamily.
Qy	851	CPSALHQLMDCWKDRNRHPKFCQIVNTLDKMRNPNLSKAMAPLSSGGINLPLDRTIP	910	DR	EMBL; BC052968; AAH52968.1; -.
Db	808	CPSALHQLMDCWKDRNRHPKFCQIVNTLDKMRNPNLSKAMAPLSSGGINLPLDRTIP	867	DR	GO; GO:0016021; C:integral to membrane; IEA.
Qy	911	DYTSFNTVDEWLEAIKMCQYKESFANAGTSFSDVVSQMMEDILRLGVLGAGHOKILNS	970	DR	GO; GO:0005524; F:ATP binding; IEA.
Db	868	DFTAFPTVDDWLSAIAKQVYRDSFLTAGFTSLQVLTQNTSEDLRLGVLGAGHOKILNS	927	DR	GO; GO:0005003; F:ephrin receptor activity; IEA.
Qy	971	IQVNRQANQIQSV 984		DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
Db	928	IHSRMVQMNQSPV 941		DR	GO; GO:0004872; F:receptor activity; IEA.
RESULT 17					GO; GO:0004687; P:protein amino acid phosphorylation; IEA.
Q72740	PRELIMINARY; PRT; 998 AA.				GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
AC	Q72740; PRT; 998 AA.				InterPro; IPR000345; Cyt_c_heme_BS.
DT	01-OCT-2003 (TrEMBLrel. 25, Created)				InterPro; IPR001090; Ephrin receptor.
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)				InterPro; IPR0003961; FN III.
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				InterPro; IPR000719; Prot_kinase.
DE	Ephrin receptor EphB3.				InterPro; IPR001660; SAM_kinase.
GN	Name=EphB3;				InterPro; IPR001245; Tyr_kinase_AS.
OS	Homo sapiens (Human).				InterPro; IPR008286; Tyr_kinase_AS.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				InterPro; IPR001426; YKase_receptorfv.
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Pfam; PF001404; Ephrin lbd; 1.
OX	NCBI_TaxID=9606;				Pfam; PF000441; fn3; 2.
RN	[1]				Pfam; PF00069; Pkinase; 1.
RP	SEQUENCE FROM N.A.				Pfam; PF00536; SAM_1; 1.
RC	TISSUE=Uterus;				ProdDom; PD001495; Ephrin_receptor; 1.
RX	MEDLINE=22388257; PubMed=12477932;				SMART; SM00615; EPH_lbd; 1.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				SMART; SM00454; SAM; 1.
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,				SMART; SM00219; Tytkg; 1.
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,				PROSITE; PS00853; FN3; 2.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				PROSITE; PS00107; PROTEIN KINASE ATP; 1.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				PROSITE; PS00109; PROTEIN KINASE DOM; 1.
RA	Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,				PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				PROSITE; PS0105; SAM_DOMAIN; 1.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,				ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Villalon D.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Fahy J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
RA	Krzyszewski M.I., Skalska U., Smalilus D.E., Schnerch A., Scheinfeld J.E.,				KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;

Qy 244 DGEWLVPIGRCMKAGFEAVENGTVCKGCPGSGTFKANKQGDACHCHPINSRTTSEBGNAC 303
Db 259 DGEWLVPIGRCMKAGFEAVENGTVCKGCPGSGTFKANKQGDACHCHPINSRTTSEBGNAC 318
Qy 304 VCRNGYRADLDPLDMCTTIPSPQAVISSVNETSLMLETTPRDSGGREDLVNLTICK 363
Db 319 TCHNPNFYRADSDSADCTTVPSPRGVSNVNETSLILEWSEPRDGLGRDLDLNNVICK 378
Qy 364 SC--GSGRGACTRCGNQVAPROGLTEPRIVISDILLAHTQYTFEIQAVNGVTDSPFS 421
Db 379 KCHGAGASACSRCDNDNVEFVQGLGTERVHSHLLAHTRTFEVQAVNGVSGKSLP 438
Qy 422 POPASVNTTNOAAPSASVIMHQVSRVDSITLSWSQDPNGVILDYELQYKEKELSEY 481
Db 439 PRYAAVNTTNOAAPSSEVPTLRHLSSSGSLTISWAPPENGVILDYEMKYFEK--SEG 496
Qy 482 NATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGMYFQMTWE-ABVQTSIOEK 540
Db 497 IASTVTSQMSVQDGLRDPARYVQVARTVAGYGRYSGMYFQMTWE-ABVQTSIOEK 556
Qy 541 LPLIIGSSAAGLVFLIAVAVIAVNCRRGPERADSEYTDKLOHYTSGHMTGPKMIVIDPF 600
Db 557 LPLIVGSATAGLVFAVAVIAVNCRRGPERADSEYTDKLOHYTSGHMTGPKMIVIDPF 612
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHKLKPKREIFVAIKLKSQYT 660
Db 613 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHKLKPKREIFVAIKLKSQYT 672
Qy 661 EKORRDLFSLASIQGDHFNHVLHGVVTKSPVMIITFEMNGSLDLSFLRQNDGQFTV 720
Db 673 EKORRDLFSLASIQGDHFNHVLHGVVTKSPVMIITFEMNGSLDLSFLRQNDGQFTV 732
Qy 721 IQLVGLMRLGTAAGKYLADNMVYHRLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 780
Db 733 IQLVGLMRLGTAAGKYLADNMVYHRLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 792
Qy 781 TSALGGKIPIRWTAPEAIQYRKFTASDVMSYGVIMMEVMSYGERPYWDMTNDQVINAIE 840
Db 793 TSALGGKIPIRWTAPEAIQYRKFTASDVMSYGVIMMEVMSYGERPYWDMTNDQVINAIE 852
Qy 841 QDRLPMPDPCPSALHQLMDCWQKDRNHRPKQIIVNTLDKMRNPNSLKAMAPISGI 900
Db 853 QDRLPMPDPCPSALHQLMDCWQKDRNHRPKQIIVNTLDKMRNPNSLKAMAPISGI 912
Qy 901 NLPLDRTIPDYSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSVMSOMMEDILRLGVTL 960
Db 913 SQPLDRTIPDYSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSVMSOMMEDILRLGVTL 972
Qy 961 AGHQKILNSIQVNRQMNQIQSVEV 986
Db 973 AGHQKILNSIQVNRQMNQIQSVEV 998
AC Q07498; STANDARD; PRT; 988 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 3 (EC 2.7.1.112) (Tyrosine-protein kinase
DE receptor CEK10) (Fragment).
GN Name=EPRB3; Synonyms=CEK10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Embryo;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;

RT "Five novel avian Eph-related tyrosine kinases are differentially
RL expressed.";
CC OncoGene 8:1807-1813(1993).
CC -I- FUNCTION: Receptor for members of the ephrin-B family.
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q07498-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07498-2; Sequence=VSP_003019;
CC Note=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Present in 10-day embryonic brain and body
CC tissues. Prominent expression in kidney. Lower expression in lung,
CC and barely detectable in brain, liver, heart, skeletal muscle and
CC thymus.
CC -I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC -I- SIMILARITY: Contains 2 fibronectin type III domains.
CC -I- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z19061; CAA79511.1; -;
DR PIR; I50611; I50611.
DR HSP; P54763; IJPA.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR007019; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_lbd_1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00853; FN3_2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01005; SAM_DOMAIN; 1.
KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW Receptor; Repeat; Transferase; Transmembrane; Tyrosine-protein kinase.
FT NON_TER. 1
FT DOMAIN <1 534 Extracellular (Potential).
FT TRANSMEM 535 555 Potential.
FT DOMAIN 556 988 Cytoplasmic (Potential).
FT DOMAIN 171 308 Cys-rich.
FT DOMAIN 312 416 Fibronectin type-III 1.
FT DOMAIN 426 518 Fibronectin type-III 2.

FT	DOMAIN	623	886	Protein kinase.
FT	DOMAIN	915	979	SAM.
FT	SITE	986	988	PDZ-binding motif (Potential).
FT	NP_BIND	629	637	ATP (By similarity).
FT	DISULFID	53	88	By similarity.
FT	BINDING	655	655	ATP (By similarity).
FT	ACT_SITE	748	748	By similarity.
FT	MOD_RES	598	598	Phosphotyrosine (by autocatalysis) (By similarity).
FT	MOD_RES	604	604	Phosphotyrosine (by autocatalysis) (By similarity).
FT	MOD_RES	782	782	Phosphotyrosine (by autocatalysis) (By similarity).
FT	MOD_RES	932	932	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CARBOHYD	323	323	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	418	418	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	558	572	Missing (in isoform Short).
FT	SEQUENCE	988 AA;	109578 MW;	/FTID=VSP_003019.
FT	SEQUENCE	988 AA;	109578 MW;	BEA0D35C03FFD3C8 CRC64;
Qy	Query Match	70.6%;	Score 3662.5;	DB 1; Length 988;
Db	Best Local Similarity	70.1%;	Pred. No. 2.9e-220;	
Db	Matches	684;	Conservative 121;	Mismatches 144; Indels 27; Gaps 5;
Qy	30	TAEIGWVHPSPGWEVSGYDENNTIRTYQVCNVFPSSQNNMLRTKFIERRGAHRHVE	89	
Db	21	TSELAWTHETGHEEVSQYDEAMNPIRTYQVCNVREANQNMLRTKFIQRQDVQRYVE	80	
Qy	90	MKFSVRDCSSIPSPGSKETFLNLYYADFSATKTFPNNMENPWKVDITIAADEFSQ	149	
Db	81	LKFTVRDCNSIPNPGSKETFLNLYYEDSDSASNSPFMENFYIKVDITIADEFSK	140	
Qy	150	VDLGRVWKINTEVRSGPVSRSFYLAPODYGCMSLIAVRVYFKCPRIIONGAIFQE	209	
Db	141	LESG-----RVNTRKVSFGLSKGFLYAFQDLGACMSLISVRAPFYKCSNTIAGFAIFPE	196	
Qy	210	TLGSAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCKMAGFEAVENTVC	269	
Db	197	TLTGAEFTSLVIAPTCIPNAVEVSFLKLYCNGDGEWVPVGNACTCAAGYEAMKDTQC	256	
Qy	270	RGCPGFTKANGQDEACTHCPINSTRTSSEGTATCVCNRYRADLPLDMPTCTIPSPAQ	329	
Db	257	QACGPGFTKQGBGCPSPNSTRTAGAATVTCICRSGFFRADADPADSACTSVPSAPR	316	
Qy	330	AVISSVNETSLMLETTPRDSGREDIVANIICKSCSGRGACTRCGDNVQYAPROL---	386	
Db	317	SVISNVNETSLVLEWSEFQDAGGRDLDLNVICKCSVERRLCSRDDNVFEFVRQLGLT	376	
Qy	387	GLTEPRIYISDLAHTQYTEIQAVNGVTPQSPSPQFASVNTTNQAAPSASIMHOVS	446	
Db	377	GLTERRIYISKVMAHPQYTEIQAVNGISSKSPYPHPFASVNTTNQAAPSAPTMHLS	436	
Qy	447	RTVDSITLSNQDPQNGVILDYEQYEKE-ISEYNATAIKGPTNTVTVOGLKAGAIYV	505	
Db	437	STGNSMTLSNTPPRNGIILDEIKYSEKQGGDIANTVTSOKNSVRLDGLKANARYM	496	
Qy	506	FOVPRARTVAGVRSKMYQMTAEAYQTSIQEKLPLIGSSAAGVFLIAVVAIYV	565	
Db	497	VQVPRARTVAGVRSYSLPTEFTQTAEDGSTSKTFOELPLVGSATAGLLFVVVIAIYV	556	
Qy	566	NRGFG-----ERADSEYTDKLQHYTSGHMTPGMKIYIDPTTYEDPNEAVR	610	
Db	557	FRKGWTEQLLSPLGRKQRNSTDPYTEKLQY-----VTPGMKYIDPTTYEDPNEAVR	612	
Qy	611	EFAKEIDISCKIEQVITGAGEFVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPFSE	670	
Db	613	EFAKEIDISCKIEVIGAGEFVCSGRLKLPGRKEIFVAIKTLKVGYTEKQRDPFSE	672	
Qy	671	ASINGQFDHNVHLEGVVTKSTPMVLIITEFMENGLSDSLRNDGQFTVQLVGMRLGI	730	
Db	673	ASINGQFDHNPNIHLEGVVTKSRPMVLIITEFMENCALDSFLRNDGQFTVQLVGMRLGI	732	

Qy	731	AAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTTYSALGKGIPI	790	
Db	733	AAGKYLSEMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDPADPTTSSLGKGIPI	792	
Qy	791	RTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYWDMTNOVDVINAIEQDYLRLPPMD	850	
Db	793	RTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYWDMTNOVDVINAIEQDYLRLPPMD	852	
Qy	851	CPSLHOLMLDCWQKDRNHRPKFGQIVNTLDKMRPNLSIKAWAPLSSGINLPDLRTIP	910	
Db	853	CPALHQLMLDCWVRDRNLRPKFAQIVNTLDKLRNAASLUKVASQSGVQSLDRTVP	912	
Qy	911	DYTSFNTVDEWLEAIKMGQYKESFANAGTSDVWSQMMEDILRLGVTLAGHKILNS	970	
Db	913	DYTFITVGVLDLAIKMGYKFNAGFVAGFASFDLVAGTAEEDLLRIGVTLAGHKILNS	972	
Qy	971	IQWRAQMNIQSVFV 986		
Db	973	IDMRLQMNQTLFVQV 988		
RESULT 19				
EPB3_HUMAN	STANDARD;	PRT;	998 AA.	
ID	EPB3_HUMAN			
AC	P54753;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor HEK-2)			
GN	Names=EPHB3; Synonyms=ETK2, HEK2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=9339063; PubMed=8397371;			
RA	Boehne B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,			
RA	Strehardt K., Ruesamen-Waigmann H.;			
RT	"PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2."			
RL	Oncogene 8:2857-2862(1993).			
CC	-1- FUNCTION: Receptor for members of the ephrin-B family. Binds to ephrin-B1 and -B2.			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- TISSUE SPECIFICITY: Ubiquitous.			
CC	-1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.			
CC	-1- SIMILARITY: Contains 2 fibronectin type III domains.			
CC	-1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.			
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DR	EMBL; X75208; CAA53021.1; --			
DR	PIR; S37627; S37627.			
DR	HSSP; P54763; IJPA.			
DR	Genew; HGNC:3394; EPHB3.			
DR	MIM; 601839; --			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.			
DR	GO; GO:0007165; P:signal transduction; TAS.			
DR	InterPro; IPR001090; Ephrin_receptor.			
DR	InterPro; IPR003962; FhIII_subd.			


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DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001560; SAM_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase AS.
DR InterPro; IPR001426; ykase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 33
FT CHAIN 34 998
FT DOMAIN 34 559
FT TRANSMEM 560 580
FT POTENTIAL 581 998
FT CYTOPLASMIC 581 998
FT CYS-RICH 199 336
FT FIBRONECTIN 340 443
FT FIBRONECTIN 453 544
FT FIBRONECTIN 633 896
FT PROTEIN_KINASE 925 989
FT SAM 996 998
FT PDZ-BINDING 996 998
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608
FT MOD_RES 614 614
FT MOD_RES 792 792
FT MOD_RES 942 942
FT CARBOHYD 351 351
FT CARBOHYD 445 445
FT SEQUENCE 998 AA; 110286 MW; 57C92C397CC61103 CRC64;

Query Match
Best Local Similarity 70.2%; Score 3661.5; DB 1; Length 998;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVEETLMDSTATAELGMMVHPSPGWEVSGYDENMNTIRYQVCN 63
Db 23 LLLPLLLPAGCRALLETLMTKWTSSELAWTSHPESGWEVSGYDENMNTIRYQVCN 82
Qy 64 VPESQNNLTKFIRRGARIRHVEKFSVRDCSSIPSPGCKETFNLYYFADPDSA 123
Db 83 VRESSQNNLTKFIRRRDVRQVVELKFTVRDCNSIPNIPGCKETFNLYYFADSDVA 142
Qy 124 TKTFNNMENPWKVDITAADESQVDLGRVMKINTEVRSGFVSRSFYLAFOYGG 183
Db 143 SASPFNNENPVKVDITAPDESRLDAG-----RVNTKVRSGFPLSKAGFYLAFOQGA 198
Qy 184 CMSLIARVFRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243

Db 199 CMSLISVRAFYKCASTTAGFALPETLTGAETPSLVIAPTCIPNAVEVPLKLYCNG 258
Qy 244 DGEWLVPGRGCMCKAGFEAVENGIVCRGCPSTGTFKANOGDEACTHCPINSETTSEGATNC 303
Db 259 DGEWVVPVGACTCATGHEPAKESQCRPCPPGSKYAKQGGPCPLPCPPNSRTTSPAASIC 318
Qy 304 VCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLETTPRDSGGRDLVYNIICK 363
Db 319 TCHNFRADSDSADSACTIVPSPRGVINSVNETSLILEWSEPRDLGVRDLDLYLVICK 378
Qy 364 SC--GSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEQAQVNGVTDQSPFS 421
Db 379 KCHGAGGASACRCDNDVEFVPRGLSEPRVHTSHLLAHTRYTFEVAQVNGVSGKSLP 438
Qy 422 POPASVNITNQAAAPSVAISMHQVSRVDSITLWSOPDOPNGVILDYELQYKEKSEY 481
Db 439 PRYAANVITNQAAAPSEVPTLRHSSGSSUTLWSAPPERNGVILDYEMKYPFK--SEG 496
Qy 482 NATAIKSPTNTVTVQGLKAGAIYVQVARTVAGYGRYSGMYPTQWTE-AEYQTSIQEK 540
Db 497 IASTVTSQMSVQLDGLRPDARYVQVARTVAGYGRYSPAEFETTSERSSGAQQLQEQ 556
Qy 541 LPLIIGSSAAGLVPLIAVVIACVNRGRFERADSEYTDKLQHYTSGHMTPGMKIYIDPF 600
Db 557 LPLIVGSATAGLVFVAVVIAIVCLRKQRHGSSEYTEKLQY----IAPGMKVYIDPF 612
Qy 601 TYEDPNEAVREFAKEIDISCVKLEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 660
Db 613 TYEDPNEAVREFAKEIDISCVKLEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 672
Qy 661 EKQRDFLSEASIMQGFDPHNVILHGVTKSTPMIITFEMENGSLDSFLRQNDGQFTV 720
Db 673 ERQERDFLSEASIMQGFDPHNVILHGVTKSTPMIITFEMENGSLDSFLRQNDGQFTV 732
Qy 721 IQLVGLRGIAAGKYLADMYVHRDLAARNILVSNLVCVKVSDFGLSRLEDDTSPTY 780
Db 733 IQLVGLRGIAAGKYLSENNYVHRDLAARNILVSNLVCVKVSDFGLSRLEDDTSPTY 792
Qy 781 TSALGGKIPRWTAPEAIQYRKTSASDVMSYGVIMVMSYGERPYWDMNQDVINAIE 840
Db 793 TSLGGKIPRWTAPEAIQYRKTSASDVMSYGVIMVMSYGERPYWDMNQDVINAIE 852
Qy 841 QYRLPPMPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSGI 900
Db 853 QYELPPMPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSGI 912
Qy 901 NLPLDRTIPDYSFNTVDWLEBAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960
Db 913 SQPLDRTVPDYTFITVGDWLDIAIKMGYKESFVSAGFASFDIVAQWTAEDLLRIGVTL 972
Qy 961 AGHQKILNSIQVRAQMNQIQSVEV 986
Db 973 AGHQKILNSIQVRAQMNQIQSVEV 998

RESULT 20
Q91YS9
ID Q91YS9 PRELIMINARY; PRT; 993 AA.
AC Q91YS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Eph receptor B3.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, and C57BL/6; TISSUE=Brain, and Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 DR EMBL; BC014822; AAH14822.1; -;
 DR EMBL; BC053085; AAH53085.1; -;
 DR HSSP; P54763; 1JPA.
 DR MGD; MGI:104770; Ephb3.
 DR GO; GO:0008046; P:axon guidance; receptor activity; IDA.
 DR GO; GO:0007411; P:axon guidance; receptor; IDA.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; FIII subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase AS.
 DR InterPro; IPR001426; Vase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00441; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM 1; 1.
 DR PRINTS; PR00014; FNTYPIII.
 DR PRINTS; PR00109; TVPKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.

SQ SEQUENCE 993 AA; 109661 MW; 07C6EF2AC98AE1B4 CRC64;
 Query Match 70.5%; Score 3657.5; DB 2; Length 993;
 Best Local Similarity 70.0%; Pred. No. 5.9e-220;
 Matches 692; Conservative 114; Mismatches 162; Indels 21; Gaps 6;
 QY 9 ALLLPLLA-----AVEETLMDSTTATAGLWGMVHPSPGSGWEEVSGYDENNTIRTYQVCN 63
 DB 15 APILLPLLLPAGCWALEETLMDTKWVTSBLAWTSHPGSGWEEVSGYDEAMNPIRTYQVCN 74
 QY 64 VFESSQNNWLRTKFIPIRRGAHRIHVEMKESVDCSSIPVPGSKETENLYYEADPDSA 123
 DB 75 VRESSQNNWLRTGFIWRREVQRYVVELKFTVDRDCNSIPNPGSKETENLYYEADSDVA 134
 QY 124 TKTFPNMNMENPVKVDVTIAADESFQVLDLGRVMKINTEVRFGPVSRSGFYLAFOYGG 183
 DB 135 SASSPFWNMENPVKVDVTIAPDESFSRLDAG----RVNTKVRSGFGLSKAGFYLAFOQGA 190
 QY 184 CMSLIAVRVYFKCPRIIQNGAIFQETLSGAEISTSLVAARGSCIANAEVDPVPIKLYCNG 243
 DB 191 CMSLSIVRAFYKKCASTTAGFALFPETLTGAEPTSLVIAPGTICIANAEVSVPLKLYCNG 250
 QY 244 DGEWLVPICRCMKAGFAVENGTVCRCGPGSGTGFKANQGDCACTHCPINSRTTSECATNC 303
 DB 251 DGEWMPVVGACTCATGHEPAAKESQCRACPPGSKAKQGEPCPCPPNSRTTSPAAIC 310
 QY 304 VCRNGYVRADLPDMPCTTIPSAQAVISSVNETSLMLEWTPPRDPSGSGREDLVYNIICK 363
 DB 311 TCHNFYRADSDSADSACTVSPPRGVISNVNETSLILEWSEPRDLGGRDLYNVICK 370
 QY 364 SCGSGRGA-----CTRCGNQVAPQLGLTPRIYISDLAHTQVTFIQAQNGVTDQS 418
 DB 371 KCRGSGAGGAPATCSRCDNVEFVPRQLGLTERRVHSHLLAHTRYTFEVOAVNGVSGKS 430
 QY 419 PESPQASVNIITNQAPSAVSIMHOVSRTVDSITLSWSQDPQNPQNVILDYELQYYEKEL 478
 DB 431 PLPRYAAVNIITNQAPSEVPTLHLHSSGSLTSLSWAPPERNGVILDYENKYYEK-- 488
 QY 479 SEYNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGMKYFQMTWE--AEYQTSI 537
 DB 489 SKGIASVTTSQKNSVQLDGLQPDARYVQVARTVAGYGOYSHPAEFETTSERGSAQQL 548
 QY 538 QEKLPLIIIGSSAAGLVFLTAIVVIAIVCNRGPERRADSEYTKLOHYTSGHMTPGMKIYI 597
 DB 549 QEOLPLIVGSTVAGFVFMVWVWVIALVCLRKQKHGPDABYTEKLOQY----TAPGMKVYI 604
 QY 598 DPFTYEDPNEAVREFPAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKS 657
 DB 605 DPFTYEDPNEAVREFPAKEIDVSCVKEEVIAGEFGEVCGRLKLPGRREVFVAIKTLKV 664
 QY 658 GYTERQRRDPLSEASIMGQFDHPNVIHLEGWVTKSTPVMITTEFMNGSLDSFLRNDGQ 717
 DB 665 GYTERQRRDPLSEASIMGQFDHPNIRLEGVVTKSRPVMILTEFMENCALDSFLRNDGQ 724
 QY 718 FTVIQVLMRLGIAAGKYLADANYVHRDLAARNILVNSNLCKVSDGFLSRLEDDTSD 777
 DB 725 FTVIQVLMRLGIAAGKYLSENNYVHRDLAARNILVNSNLCKVSDGFLSRLEDDTSD 784
 QY 778 PTVTSALGGKIPIRWTAPEAIOYRKFTSASDVMSYGIVMWEVMSYGERPYPWDMTNDQVIN 837
 DB 785 PTVTSALGGKIPIRWTAPEAIAIYRKFTSASDVMSYGIVMWEVMSYGERPYPWDMNSQDVIN 844
 QY 838 AIEQYRLPPPMDCPSALHQLMDCWKORNRHHPKFGQIVNTLDDKMRNPNSLKAMAPLS 897
 DB 845 AVEODYRLPPPMDCPTALHQLMDCWVRDRNLRPKEFSQIVNTLDDKLRNAASLKVTASAP 904
 QY 898 SGINPLLDRTYIDYTSFNTVDEWLEAIKMGQVKESFANAGFTSDVVSOMMEDILRLG 957
 DB 905 SGMSQPLLDRTYIDYTFVTGOWLDKMRGKRYKESFVGAGFASFDLVAQMTAEDLRLG 964
 QY 958 VTLAGHOKKILNSIQVMRAQMNQISVEV 986
 DB 965 VTLAGHOKKILCSIQDMRLQMNQTLFPQV 993

RESULT 21
 ID EPB3_MOUSE STANDARD; PRT; 993 AA.
 AC P54754, Q62214;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor MDK-5) (Developmental kinase 5) (SEK-4).
 GN Name=Ephb3; Synonyms=Eck2, Mdk5, Sek4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Embryo;
 RX MEDLINE=96074837; PubMed=7478528;
 RA Clossok T., Lerch M.M., Ullrich A.;
 RT "Cloning, characterization, and differential expression of MDK2 and
 RT MDK5, two novel receptor tyrosine kinases of the eck/eph family.";
 RL Oncogene 11:2085-2095 (1993).
 RN [2]
 RP SEQUENCE OF 719-993 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=95034306; PubMed=7947319;
 RA Becker N., Seitanidou T., Murphy P., Mattei M.-G., Topilko P.,
 RA Nieto A., Wilkinson D.G., Charnay P., Gilarli P.;
 RT "Several receptor tyrosine kinase genes of the Eph family are
 RT segmentally expressed in the developing hindbrain.";
 RL Mech. Dev. 47:3-17 (1994).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410 (2000).
 CC -1- FUNCTION: Receptor for members of the ephrin-B family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in cells of the retinal ganglion
 CC cell layer during retinal axon guidance to the optic disk.
 CC -1- SIMILARITY: Belongs to the tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z49086; CAA89910.1; -;
 DR EMBL; X76012; CAA53599.1; -;
 DR PIR; I48653; I48653.
 DR PIR; I48761; I48761.
 DR HSP; P54763; IJPA.
 DR MGD; MGI:104770; Ephb3.
 DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
 DR GO; GO:0007411; P:axon guidance; IDA.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR008979; Gal_bind_like.

DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYFKG; 1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 29 Potential
 FT CHAIN 30 993 Ephrin type-B receptor 3.
 FT DOMAIN 30 554 Extracellular (Potential).
 FT TRANSMEM 555 575 Potential.
 FT DOMAIN 576 993 Cytoplasmic.
 FT DOMAIN 191 328 Cys-rich.
 FT DOMAIN 332 438 Fibronectin type-III 1.
 FT DOMAIN 448 539 Fibronectin type-III 2.
 FT DOMAIN 628 891 Protein kinase.
 FT DOMAIN 920 984 SAM.
 FT SITE 991 993 PDZ-binding motif (Potential).
 FT NP_BIND 634 642 ATP (By similarity).
 FT BINDING 660 660 ATP (By similarity).
 FT ACT_SITE 753 753 By similarity.
 FT MOD_RES 603 603 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 609 609 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 787 787 Phosphotyrosine (by autocatalysis)
 FT (Potential).
 FT MOD_RES 937 937 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT CARBOHYD 343 343 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 440 440 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 719 719 R -> Q (in Ref. 2).
 SQ SEQUENCE 993 AA; 109585 MW; 0B66A4D391266C79 CRC64;
 Query Match 70.0%; Score 3630.5; DB 1; Length 993;
 Best Local Similarity 69.8%; Pred. No. 2.9e-218;
 Matches 690; Conservative 113; Mismatches 165; Indels 21; Gaps 6;
 QY 9 ALLLLPILA-----AVETLMDSTTATAEIGWVHPSPSGWEEVSGYDENNTTIRTYQVCN 63
 DB 15 APLLPPLLPPAGCWALEETLMDTKWVTSALWTSHPESGWEEVSGYDENNTTIRTYQVCN 74
 QY 64 VPSSQNNWLRTRKFIIRRGAAHRTHEVMKFSVRDSSIPSPVPSGCKETFNLYYEADPDSA 123
 DB 75 VRESSQNNWLRTRGFIWRREVQRYVELKFTVRDNCISIPNIPGSKETFNLYFEASDVA 134
 QY 124 TKTFPNNMENPWVKVDITIAADESFSQVDLGGRYVKINTEVRSFGPVSRSFGYLAFOQYGG 183
 DB 135 SASSPFWMENPYVKVDITAPDESFSRLDAG----RVNTKRSFGPLSKAGFYLAFOQGA 190
 QY 184 CMSLIAVRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVIFKLYCNG 243
 DB 191 CMSLISVRAGDKKCASTTAGFALPETLTGAETPSLVIAFGTCTIANAEVSVPLKLYCNG 250

FT	ACT_SITE	662	By similarity.
FT	MOD_RES	512	Phosphotyrosine (by autocatalysis)
FT		518	(Potential).
FT	MOD_RES	518	Phosphotyrosine (by autocatalysis)
FT		518	(Potential).
FT	MOD_RES	596	Phosphotyrosine (by autocatalysis)
FT		596	(Potential).
FT	MOD_RES	846	Phosphotyrosine (by autocatalysis)
FT		846	(Potential).
FT	CARBOHYD	252	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	344	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	398	N-linked (GlcNAc. . .) (Potential).
FT	SEQUENCE	902 AA; 100850 MW; CCBABF7D39273CA CRC64;	
Query Match			
Best Local Similarity 73.2%; Score 3612.5; DB 1; Length 302;			
Matches 658; Conservative 127; Mismatches 109; Indels 5; Gaps 3;			
Qy	84	HRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEAD--FDSATYTFPWNWNPWKVDTTI	141
Db	1	HRVYVENRFTVRDCSSLPNVPSCKETFNLYYYETDSNDKISTF--WNESPLYKVDTTI	58
Qy	142	AADESFSQVDLGGKVMKINTEVRSGFVSRSGFYLAQDYGGMSLIAVRVFKKCPRII	201
Db	59	AADESFSQVDLGGKVMKINTEVRSGFVSRSGFYLAQDYGGMSLSLVRVFKKCPSVV	118
Qy	202	QNGAIFQETLSGAESTSLVAARGSCIANABEVDVPIKLYCNGDGEWLVPIGRCMKAGFE	261
Db	119	QNFVAVFETWTGAESTSLVIARGTCIPNABEVDVPIKLYCNGDGEWLVPIGKCTCKAGYE	178
Qy	262	AVENGTVCRGCPSTFKANGDDEACTHCPIINSRTSGATNCVCRNGYRADDLPDMPC	321
Db	179	P-ENHVYVCKACPAAMFRANQMGICCAQCPANSRSTSEASPIICRNGYRADDFTPEAPC	237
Qy	322	TTTSPAQVATSSVNETSLMLEWTPRDSGREDLVNIICKSCSGRGACTRCGDNVQY	381
Db	238	TSPVSGPRNVISIVNETAITLEWHPPTGTRDDVNIICKCQSDRRGCSHDDNDVF	297
Qy	382	APROLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSQFASVNIITNQAPSAVSI	441
Db	298	VPRLGLTDFVFLSNLWVHTPYTFEIQAVNGVTKSPFPFQHVSVNIITNQAPSSVPI	357
Qy	442	MHVSRVTVDITLSWSPQDQNGVILDYELQYKEKSEYNATAIKSPNTVTVOGLKAG	501
Db	358	MHVQKATWKSITLWSPQEPQNGIILDYELQYKEKSEYNATAIKSPNTVTVOGLKAG	417
Qy	502	AIYVFOVRAITVAGYRGYSGMYFOTWEAYQTSIOEKPLIITGSSAAGLVFLIAVVI	561
Db	418	VVVVVQVRAITVAGYRGYSGMYFOTWEAYQTSIOEKPLIITGSSAAGLVFLIAVVI	477
Qy	562	AIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTVEDPNEAVRFAKEIDISCV	621
Db	478	SIVCSRKRTYSKEAVYSDKLOHYTSGRSGPMKIYIDPFTVEDPNEAVRFAKEIDISCV	537
Qy	622	KIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTERQRDFLSEASIMQFDPHN	681
Db	538	KIEEVIGAGEFGEVYKRLKLPKREISVAIKTLKAGYSEKQRDFLSEASIMQFDPHN	597
Qy	682	VIHLEGVTKSTPMIITFENSGSLDFLRNDQGTIVQLVCMRGIAGMKYLADMN	741
Db	598	IIRLEGVTKSRPMIITFENMGALDFLRNDQGTIVQLVCMRGIAGMKYLSEMN	657
Qy	742	VVHRDLARNILVNSLVCKYDFGLSRFLRDEDDTSDPTYSALGKPIRWTAPETAQYR	801
Db	658	VVHRDLARNILVNSLVCKYDFGLSRFLRDEDDTSDPTYSALGKPIRWTAPETAQYR	717
Qy	802	KFTSASDWSYGIYVMEVMSYGERPYWDMTNQDVINAIEQDYRLPPPPMDPCPSALHQLMLD	861
Db	718	KFTSASDWSYGIYVMEVMSYGERPYWDMSNQDVINAIEQDYRLPPPPMDPCPSALHQLMLD	777
Qy	862	CWQKDRNHRPKFGQIVNTLDKMIINPNLSKMAPLSSGNIPLLDRIPIDYTSFNTVDWE	921
Db	778	CWQKDRNHRPKFGQIVNTLDKMIINPNLSKMAPLSSGNIPLLDRIPIDYTSFNTVDWE	837

Qy 922 LEAKMGQYKESFANAGFTFDVVVSOMMEDILRLGTVTLAGHOKKILNSIQWRAQMNQ 980
Db 838 LSAIKMGQYRDNFLSSGFTSLHVVAQMTSEDLRIGITLAGHOKKILNSIQWRAQMNQ 896

RESULT 23

Q6NRE9 PRELIMINARY; PRT; 974 AA.
ID Q6NRE9 AC Q6NRE9; 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
MSDL=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
MSDL=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.,
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
MSDL=22341132; PubMed=12454917;
RA Klein S., Strausberg R.,
Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
receptor subfamily.
EMBL; BC070804; AAH70804.1; .
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR01660; SAM.
DR InterPro; IPR011510; SAM_2.

759 VCKVSDPGLSRPLEDDTSDPYTTSALGCKPIPIRTWTAPEAIQYRKFTSASDVWSYGLVMWE 81

711 VCKVSDPGLSRPLEDDTSDPYTTSALGCKPIPIRTWTAPEAIQYRKFTSASDVWSYGLVMWE 770

819 VMSYGERPVDWMTNODVINAIEQDYRLPPPPMDPCPSALHQLMLDCWOKDRNHRKFGQIVN 878

771 VMSYGEQPPVWMSNQDDINAVEQDYRLPPPPMDPCPSALHQLMLDCWOKDRNHRKFGQIVN 830

879 TLDKMTIRNPNSLKAMAPLSSGINULPLDRTIPDTSFNTVDEWLEAIKMGQYKESFANAG 938

831 TLDKLIIRNAASLKVTASAPSGMSQPLDRTVPDYTTTTCGDLMDALIKMRYKESFVGAG 890

939 FTFSFDVWSOMMEDILRLGVTILAGHOKKILNSIQVMRAQNNQTSVEZ 986

891 FASFDFLVAQMTAEEDLLRIGVTILVGHQKKILCSIQDMLQNNQTLFVQV 938

RESULT 28

EPB5 CHICK

ID ID EPB5 CHICK STANDARD; PRT; 1002 AA.

AC Q07497;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ephrin type-B receptor 5 precursor (BC 2.7.1.112) (Tyrosine-protein kinase CEK9).

GN Name=EPHB5; Synonyms=CEK9;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=97066069; PubMed=8905550;

RA Soans C., Holash J.A., Pavlova Y., Pasquale E.B.;

RT "Developmental expression and distinctive tyrosine phosphorylation of the Eph-related receptor tyrosine kinase Cek9.;"

RT J. Cell Biol. 135:781-795(1996).

[2]

PARTIAL SEQUENCE FROM N.A.

RP MEDLINE=93288394; PubMed=8510926;

RA Sajjadi F.G., Pasquale E.B.;

RT "Five novel avian Eph-related tyrosine kinases are differentially expressed.;"

RT Oncogene 8:1807-1813(1993).

CC -!- FUNCTION: Receptor for members of the ephrin-B family.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Most abundant in thymus and detectable in brain, retina, kidney, lung and heart. Not detected in skeletal muscle and liver.

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.

CC -!- SIMILARITY: Contains 2 fibronectin type III domains.

CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.

CC -----

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CC -----

DR EMBL; U23783; AAB41054.1; --

DR HSSP; P54763; IJPA.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001090; Ephrin_receptor.

DR InterPro; IPR003962; FNIII_subd.

DR InterPro; IPR003961; FN III.

"Spatially regulated expression of three receptor tyrosine kinase genes during gastrulation in the zebrafish.";
Development 120:287-299(1994).

RT SEQUENCE FROM N.A.
RA Brennan C.H., Xu Q., Sordino P.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF369382; AAK54726.1; -.
DR HSP; P54763; IJPA.
DR GO: 0016020; C:membrane; IEA.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0005003; F:ephrin receptor activity; IEA.
DR GO: 0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0016740; P:transferase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003962; FhIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR001426; Y_kase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00014; ENTPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TVR; 1.
DR PROSITE; PS00791; RECEPTOR TVR_KIN_V_2; 1.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 523 AA; 101719 MW; 30DD8B1C87239790 CRC64;

Query Match 62.4%; Score 3235; DB 2; Length 923;
Best Local Similarity 61.8%; Pred. No. 1.4e-193;
Matches 603; Conservative 138; Mismatches 173; Indels 62; Gaps 4;

QY 11 LLLPLLAAREETLMDSTATAELGMMVHPSPGHEEVSVDENWNTIYQVNCVFPESON 70
DB 10 LWPVILAAVEETLMDSRWATTELAWTTPESGHEEVSVDHLLPIYQVNLSPNQN 69

QY 71 NWLRTKIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADPDSATKTPPNW 130
DB 70 NWLRTDIPRGVLVYVELKFSVRDCGSIPIPIGSKETFNLYYESDGMATASPPW 129

QY 131 MENPWVKVDITAADESPQDLGRVMKINTEVRSFGVSRSGFYLAQDYGGCMLIAV 190
DB 130 RENPVYKVDITAPDESPSLLESQ---IVNTKVSFGPLSKAGFYLAQDLGACMSLISA 185

QY 191 RVYRKCPRIIONCAIQETLSGAESTSIYAARGSCIANAEEDVDVPIKLYCNGDGLVP 250
DB 186 RVFPKCKSTSIANFAPFETATGAETSLVIAAGCPVNAEBSVPLKLYCNGDGMWVP 245

QY 251 IGRCMCKAGFAEVENGVVCGPCSGTEPKANQGEACHTCPINSRTTSEGATNCVCRNGY 310
DB 246 VGACTCMPGEPAPKDTQCACTPCTFKSKQGECSMPCFSNRSRASSVCFQSGYY 305

QY 311 RADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVNIICKSCSGGR 370
DB 311 RADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVNIICKSCSGGR 370

Db 306 RADSLDPLDTACTTVPSPALNVISSVNETSVLEWSEPRDSGGRGDVVYVNVCKKCLHDGG 365
QY 371 ACTRCGDNVOYAPROLGLTEPRIYISDLAAHTQYTEIOAVNGVTDQSPSPFASVNIIT 430
Db 366 SCARCDNNEVSPRRIGLAERQAANLNLOQAHYSEIOAVNGVSPKSPSPQITVNIIT 425
QY 431 TNOAAPSAVISIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKELSEYNATAIKSPT 490
Db 426 TNOAAPSAVPTVHLMEATAGTSLSLWLPPEPNGVILDEYIKYQER--GESFSTVTVAQH 483
QY 491 NTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFOTWTEAEYQTSIQKLPILIISSAA 550
Db 484 TSAKVEGLKAGTVYSVQVARTVAGYGRYSNPNVDFSTLSYDDPERVQDLLPLIVGSASA 543
QY 551 GLVFLTAUVVIAIVCNRRGFERADSEYTDKLQHYTSGHMTPGMKIYIDPTFYEDPNEAVR 610
Db 544 GFVILAMIVIAVVCURRORTSELSYTEKLOQYVS---PGVKYVIDPTFYEDPNEAVH 599
QY 611 EFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKLKSQYTEKQRDFLSE 670
Db 600 EFARKIDISCVKIEKVI GAGEFGEVCRGLKQAGRKETTVAIKLKAGYTEHQRRDFLSE 659
QY 671 ASIMGQFHPNVHLGVVTKSTPVMITTEPMENGSLDSFLRQNDGQFTVQLVGLRGI 730
Db 660 ASIMGQFHPNVHLGVVTRSCPVLIVTEFMENGALDSFLRNDGRFTVQLVGLRGI 719
QY 731 AAGMKYLADMYVHRDLAARNILVNSLVCKVSDGFLSRFLEDDTSDPTVTSALGGKPI 790
Db 720 AAGMKYLSDMYVHRDLAARNVLVNSLMCKVSDGFLSRFLDSDPTVTSALGGKPI 779
QY 791 RWTAPETAIQYRKFTSASDVMSYGI VNMVMSYGERPYWDMTQDVINAIEQDYRLPPMD 850
Db 780 RWTAPETAIARFKFTSASDVMSYGI VNMVMSYGERPYWDMTQDVINAIEQDYRLPPMD 839
QY 851 CPALHQLMLDCWQKORNRHPRFGQIVNTLDMKIRNPNSLKAWAPLSSGINLPLDRTIP 910
Db 840 CPALHQLMLECWVKEKRNMRPRFGQIVSTLDKLLRNAASLKVLTSTHSG----- 888
QY 911 DYTSEFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTLAGHQKILNS 970
Db 889 -----DLCRIGGTLPGHQRKSIDG 907

QY 971 IQVMRAQNMNQIQSVVEV 986
Db 908 AQDIKQMSQTLPIRV 923

RESULT 30
EP4A_XENLA STANDARD; PRT; 986 AA.
ID EP4A_XENLA
AC Q91845;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 4A precursor (EC 2.7.1.12) (Tyrosine-protein kinase receptor SEK-1) (XSEK-1).
GN Name=SEK1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125143; PubMed=8575301;
RA Xu Q., Allard G., Holder N., Wilkinson D.G.;
RT "Expression of truncated sek-1 receptor tyrosine kinase disrupts the segmental restriction of gene expression in the Xenopus and zebrafish hindbrain".
RL Development 121:4005-4016(1995).
CC -!- FUNCTION: Receptor for members of the ephrin-A family. Required for interactions that regulate the segmental identity or movement of cells (By similarity).

CC CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC CC tyrosine phosphate.
 CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC CC -!- DEVELOPMENTAL STAGE: Expression occurs in R3, R5 and transiently
 CC CC at lower levels in R2.
 CC CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC CC receptor subfamily.
 CC CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC CC or send an email to license@ebi.ac.uk).
 CC CC -----
 CC CC EMBL; X91191; CAA62601.1; -;
 CC CC HSSP; P54763; 1JUPA.
 CC CC InterPro: IPR006209; EGF like.
 CC CC InterPro: IPR001090; Ephrin receptor.
 CC CC InterPro: IPR003962; FNIII Subd.
 CC CC InterPro: IPR003961; FN III.
 CC CC InterPro: IPR008957; FN III-like.
 CC CC InterPro: IPR008979; Gal bind like.
 CC CC InterPro: IPR009030; Grow fac recept.
 CC CC InterPro: IPR011009; Kinase like.
 CC CC InterPro: IPR00719; Prot_kinase.
 CC CC InterPro: IPR001660; SAM.
 CC CC InterPro: IPR001245; Tyr_pkinase.
 CC CC InterPro: IPR008266; Tyr_pkinase AS.
 CC CC InterPro: IPR001426; Ykase receptor.
 CC CC Pfam; PF00404; Ephrin_lbd; 1.
 CC CC Pfam; PF00041; fn3; 2.
 CC CC Pfam; PF00069; Pkinase; 1.
 CC CC Pfam; PF00536; SAM; 1.
 CC CC PRINTS; PR00014; FNTYPEIII.
 CC CC PRINTS; PR00109; TYRKINASE.
 CC CC ProDom; PD001495; Ephrin receptor; 1.
 CC CC ProDom; PD000001; Prot_kinase; 1.
 CC CC SMART; SM00615; EPH_lbd; 1.
 CC CC SMART; SM00060; FN3; 2.
 CC CC SMART; SM00454; SAM; 1.
 CC CC SMART; SM00219; TyrKc; 1.
 CC CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
 CC CC PROSITE; PS00853; FN3; 2.
 CC CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 CC CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC CC PROSITE; PS00790; RECEPTOR TYR_KIN_V_1; 1.
 CC CC PROSITE; PS00791; RECEPTOR TYR_KIN_V_2; 1.
 CC CC PROSITE; PS00105; SAM_DOMAIN; 1.
 CC CC ATP-binding; Glycoprotein; Receptor; Repeat; Signal;
 CC CC Transferrase; Transmembrane; Tyrosine-protein kinase.
 CC CC SIGNAL 1 20
 CC CC CHAIN 21 966
 CC CC DOMAIN 21 547
 CC CC TRANSMEM 548 569
 CC CC POTENTIAL.
 CC CC Cytoplasmic (Potential).
 CC CC Cys-rich.
 CC CC Fibronectin type-III 1.
 CC CC Fibronectin type-III 2.
 CC CC Protein kinase.
 CC CC SAM.
 CC CC PDZ-binding motif (Potential).
 CC CC ATP (By similarity).
 CC CC ATP (By similarity).
 CC CC By similarity.
 CC CC Phosphotyrosine (by autocatalysis) (By
 CC CC similarity).
 CC CC Phosphotyrosine (by autocatalysis) (By
 CC CC similarity).
 CC CC MOD_RES 601 601

FT	MOD_RES	778	778	Phosphotyrosine (by autocatalysis) (Potential).
FT	MOD_RES	928	928	Phosphotyrosine (by autocatalysis) (Potential).
FT	CARBOHYD	340	340	N-linked (GlcNAc..) (Potential).
FT	CARBOHYD	407	407	N-linked (GlcNAc..) (Potential).
SQ	SEQUENCE	986 AA; 109840 MW; C34F4078D3F025F CRC64;		
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Best Local Similarity 60.28; Pred. No. 3.8e-184;				
Matches 583; Conservative 148; Mismatches 218; Indels 20; Gaps 10;				
Qy	18	AVETLMDSTATAELGMMVHP-PSGWEVSGVDNNTTIRTYQVCNVFSSQNNWLRTK	76	
Db	28	ASEVTLDSRSVQELGASIAPIEGGWEVSIIMDEKNTPIRTYQVCNVFSSQNNWLRTD	87	
Qy	77	FIRRGAAHRTHEVMEKFSVRDCSSIPSPGSKETFNLYYEADPDSATKTFPNWMEPMW	136	
Db	88	WIPRSGAQRVYVRIKFTLRDCNSLPGVNGTKETFNLYYESNNDKERFI-----RETQYV	143	
Qy	137	KVDTIAADESFSVDLGGVRVWKINTEVSRGVPVRSRSGFYLAFOYGGCMSLIAVVRVYRK	196	
Db	144	KIDTIAADESFTQVDIGDIRIMKLNTEVDVGPLSKGKGYLAFOVDGACIALVSVRVYKK	203	
Qy	197	CPRIQNGAIFQETLGAESTSLVAARGSCIANAEVDVPKLYCNGDGEWLVPICRMC	256	
Db	204	CPLTVRNLAQFPDITIGSDTSLVEVRGSCVDNSEKQVP-KMYCGADGEWLVPICNCLC	262	
Qy	257	KAGFEAVENGTVRCGSPSGTFKANOGEACHTHCPIINSRTTSEGATNCVCRNGYRADLDP	316	
Db	263	NAGFEEHNGG--CQACKVGYKALSTDAACSKCPPHSYALREGSTCTCGRYFRADTDP	320	
Qy	317	LDMPCTTIPSAPOAVISSVNETSLMLEWTTPRSGGREDLVNIIICKSCSGRCACTRCG	376	
Db	321	ASMPCTPPSPAPQNLISNNVNETSVNLEWSPQSGGPRDVSYNLVCRCCGDLTRCPG	380	
Qy	377	DNVQYAPQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDPQSPSPQFASVNIITNQAAP	436	
Db	381	SGVHSPQNGLTKTKVSIITDLQAHNTYTFEVSINGVSKQNPQDQAVSVVTITNQAAP	440	
Qy	437	SAYSIMHQVSRVDSITLSWSPQDPQNGVILDVLYEKELSHYNATAIKSPNTVTVQ	496	
Db	441	STVTIQPKDITRHSVSLTWPEPERNGVILEYEVKYEKDQNERTYRIVKTTSRSDIK	500	
Qy	497	GLKAGALYVFOVRARTVAGYSGKMYFOTMTAEAYQTSIQEKLPLIIGSSAAGLVFLI	556	
Db	501	GLNPLTAYVHVHARTAAAGGEGFSGPPEFTNTVPSPMIG-EGASPTVLVSVAGSIVLV	559	
Qy	557	AVVIAIVCNRR--GFERADSEYTDKLQHYTSGHMTFGMKIYIDPFTYEDPNEAVREFAK	614	
Db	560	VILIAAFVISRRSKYSKAKQEADEE-----KHLNQGVKTVYDPTVEDPQAVREFAK	613	
Qy	615	EIDISCVKIQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDFLSEASIM	674	
Db	614	EIDASCIIKIKVIGVGEFGEVCSGRLKVPKREIYVAIKTLKAGYTDKQRDFLSEASIM	673	
Qy	675	GFDPHPVHLEGVVTYKSTPVMITPEMENGSLDSFLRQNDGQFTVLQVLMRLGIAAGM	734	
Db	674	GFDPHPNIIHLEGVVTYKCKPVMITEWENGSLDAFLRKNDGRTVLQVILRGISGM	733	
Qy	735	KYLADMYVHRDLAARNILVNSNLVCKVSDPGLSRFLDDTSDPTTYSALGGKIPIRWTA	794	
Db	734	KYLSMSYVHRDLAARNILVNSNLVCKVSDPGLSRVLEDD-PEAAYTTR-GGKIPIRWTA	791	
Qy	795	PEAIQYRKFTSASDVMSYIGIWMVMSYGERPVDWNTQVDVNNIIEOYDLRPPMDCPSA	854	
Db	792	PEAIAYRKFTSASDVMSYIGIWMVMSYGERPYWMSNQDVVKAIEEYGLRPPMDCPIA	851	
Qy	855	LHQLMLDCWOKDRNHRPKFGQIVNTLDMKIRNPNLSKAMA-PLSSGGLNPLDRTIDYT	913	
Db	852	LHQLMLDCWOKERSDRPKFGQIVSMLDKLIARNPNLSKARTGLDSSRTNTTLDPSSSEWS	911	
Qy	914	SFNTVDEWLEAIKMGQYKESFANAGTFSFDVVSQMMMEDILRLGVTLAGHOKILNSIQV	973	

Db 912 QVASVLDWLQAIKMYKDNFTAAGYTSLEAVVHVNQDDLTRIGISSPSHQNKILSSVQG 971
QY 974 MRAQMNQIQ 982
Db 972 MRTOMQQIQ 980

Search completed: December 30, 2004, 16:49:57
Job time : 221 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 16:43:36 ; Search time 157 Seconds
(without alignments)

2259.182 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRRIGALLLLPLLAIVE.....ILNSIQVMRAQMNIQSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5181	99.9	1055	16	US-10-648-593-139
2	5181	99.9	1055	17	US-10-757-262-100
3	5181	99.9	1055	17	US-10-768-158-8
4	5171.5	99.7	987	14	US-10-295-027-1193
5	4993.5	96.3	995	15	US-10-029-020-62
6	3934.5	75.8	984	15	US-10-029-020-60
7	3670.5	70.7	998	14	US-10-295-027-1183
8	3670.5	70.6	998	17	US-10-783-528-112
9	3661.5	70.6	998	14	US-10-354-358-4
10	3661.5	70.6	998	17	US-10-723-860-2850
11	3661.5	70.6	1007	15	US-10-276-774-2273
12	3603.5	69.5	993	14	US-10-187-958-1
13	3594.5	69.3	896	16	US-10-408-765A-2942
					Sequence 139, App
					Sequence 100, App
					Sequence 8, Appli
					Sequence 119, Ap
					Sequence 62, Appl
					Sequence 60, Appl
					Sequence 1183, Ap
					Sequence 112, App
					Sequence 4, Appli
					Sequence 2850, Ap
					Sequence 2273, Ap
					Sequence 1, Appli
					Sequence 2942, Ap

14	3075.5	59.3	985	15	US-10-029-020-61	Sequence 61, Appl
15	3053	58.8	991	10	US-09-823-187-44	Sequence 44, Appl
16	3048	58.8	953	14	US-10-412-277-7	Sequence 7, Appli
17	3045	58.7	986	17	US-10-723-860-597	Sequence 597, App
18	3038.5	58.6	993	10	US-09-823-187-39	Sequence 39, Appl
19	3038.5	58.6	993	10	US-09-823-187-41	Sequence 41, Appl
20	3038	58.6	1104	9	US-09-982-610-36	Sequence 36, Appl
21	3036	58.5	1037	14	US-10-316-124-3	Sequence 3, Appli
22	3036	58.5	1037	14	US-10-353-690-40	Sequence 40, Appl
23	3031	58.4	975	14	US-10-412-277-8	Sequence 8, Appli
24	3028	58.4	998	10	US-09-823-187-40	Sequence 40, Appl
25	3013	58.1	998	10	US-09-823-187-42	Sequence 42, Appl
26	3013	58.1	998	10	US-09-823-187-43	Sequence 43, Appl
27	2930.5	56.5	983	9	US-09-771-161A-227	Sequence 227, App
28	2930.5	56.5	983	14	US-10-205-823-97	Sequence 97, Appl
29	2930.5	56.5	983	14	US-10-345-680-2	Sequence 2, Appli
30	2930.5	56.5	983	14	US-10-295-027-602	Sequence 602, App
31	2930.5	56.5	983	15	US-10-029-020-59	Sequence 59, Appl
32	2928	56.4	968	14	US-10-412-277-6	Sequence 6, Appli
33	2923	56.3	1005	15	US-10-029-020-63	Sequence 63, Appl
34	2844	54.8	1276	9	US-09-982-610-24	Sequence 24, Appl
35	2838	54.7	1036	14	US-10-220-955-21	Sequence 21, Appl
36	2835	54.6	1036	10	US-09-971-708-2	Sequence 2, Appli
37	2835	54.6	1036	14	US-10-245-752-104	Sequence 104, App
38	2835	54.6	1036	14	US-10-245-859-104	Sequence 104, App
39	2835	54.6	1036	14	US-10-245-103-104	Sequence 104, App
40	2835	54.6	1036	14	US-10-245-107-104	Sequence 104, App
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42	2835	54.6	1036	14	US-10-245-771-104	Sequence 104, App
43	2835	54.6	1036	14	US-10-245-851-104	Sequence 104, App
44	2835	54.6	1036	14	US-10-245-883-104	Sequence 104, App
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55	2835	54.6	1036	14	US-10-243-024-104	Sequence 104, App
56	2835	54.6	1036	14	US-10-243-409-104	Sequence 104, App
57	2835	54.6	1036	14	US-10-245-621-104	Sequence 104, App
58	2835	54.6	1036	14	US-10-245-880-104	Sequence 104, App
59	2835	54.6	1036	14	US-10-245-033-104	Sequence 104, App
60	2835	54.6	1036	14	US-10-243-095-104	Sequence 104, App
61	2835	54.6	1036	14	US-10-245-185-104	Sequence 104, App
62	2835	54.6	1036	14	US-10-245-427-104	Sequence 104, App
63	2835	54.6	1036	14	US-10-245-473-104	Sequence 104, App
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65	2835	54.6	1036	14	US-10-245-877-104	Sequence 104, App
66	2835	54.6	1036	14	US-10-246-976-104	Sequence 104, App
67	2835	54.6	1036	14	US-10-243-320-104	Sequence 104, App
68	2835	54.6	1036	14	US-10-242-743-104	Sequence 104, App
69	2835	54.6	1036	14	US-10-242-845-104	Sequence 104, App
70	2835	54.6	1036	14	US-10-238-325-104	Sequence 104, App
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73	2835	54.6	1036	14	US-10-238-411-104	Sequence 104, App
74	2835	54.6	1036	14	US-10-243-124-104	Sequence 104, App
75	2835	54.6	1036	14	US-10-243-425-104	Sequence 104, App
76	2835	54.6	1036	14	US-10-243-446-104	Sequence 104, App
77	2835	54.6	1036	14	US-10-245-874-104	Sequence 104, App
78	2835	54.6	1036	14	US-10-242-653-104	Sequence 104, App
79	2835	54.6	1036	14	US-10-243-167-104	Sequence 104, App
80	2835	54.6	1036	14	US-10-243-388-104	Sequence 104, App
81	2835	54.6	1036	14	US-10-244-947-104	Sequence 104, App
82	2835	54.6	1036	14	US-10-244-968-104	Sequence 104, App
83	2835	54.6	1036	14	US-10-244-990-104	Sequence 104, App
84	2835	54.6	1036	14	US-10-245-079-104	Sequence 104, App
85	2835	54.6	1036	14	US-10-245-127-104	Sequence 104, App
86	2835	54.6	1036	14	US-10-245-207-104	Sequence 104, App

87 2835 54.6 1036 14 US-10-245-646-104 Sequence 104, App
88 2835 54.6 1036 14 US-10-245-695-104 Sequence 104, App
89 2835 54.6 1036 14 US-10-245-699-104 Sequence 104, App
90 2835 54.6 1036 14 US-10-245-737-104 Sequence 104, App
91 2835 54.6 1036 14 US-10-245-878-104 Sequence 104, App
92 2835 54.6 1036 14 US-10-245-890-104 Sequence 104, App
93 2835 54.6 1036 14 US-10-245-899-104 Sequence 104, App
94 2835 54.6 1036 14 US-10-245-900-104 Sequence 104, App
95 2835 54.6 1036 14 US-10-247-058-104 Sequence 104, App
96 2835 54.6 1036 14 US-10-245-454-104 Sequence 104, App
97 2835 54.6 1036 14 US-10-237-471-104 Sequence 104, App
98 2835 54.6 1036 14 US-10-238-261-104 Sequence 104, App
99 2835 54.6 1036 14 US-10-238-324-104 Sequence 104, App
100 2835 54.6 1036 14 US-10-241-860-104 Sequence 104, App

ALIGNMENTS

RESULT 1
US-10-648-593-139
; Sequence 139, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 139
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-139

Query Match 99.9%; Score 5181; DB 16; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALRRLLGALLLLPDLAAVEETLMDSTTATAEIGCMVHPSPGWEVSGYDENMTITTYQ 60
Db 1 MALRRLLGALLLLPDLAAVEETLMDSTTATAEIGCMVHPSPGWEVSGYDENMTITTYQ 60
Qy 61 VCNVPESSONNLTKTIRRRGAHRHIVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADF 120
Db 61 VCNVPESSONNLTKTIRRRGAHRHIVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADF 120
Qy 121 DSATKTFNNMNMWPKVDTTAADESPQVLDGRVKNKINTEVRSFGPVSRSGLYAFQD 180
Db 121 DSATKTFNNMNMWPKVDTTAADESPQVLDGRVKNKINTEVRSFGPVSRSGLYAFQD 180
Qy 181 YGGCNSLIANVFRKCPRIITONGAIPOETLSGAESTSLVAARGSCITANAEEDVPIKLY 240
Db 181 YGGCNSLIANVFRKCPRIITONGAIPOETLSGAESTSLVAARGSCITANAEEDVPIKLY 240
Qy 241 CNGDEWLVPICRCMKAGFAVENGTVCRCPSGTTFKANOGDEACTHCPINSRTTSEGA 300
Db 241 CNGDEWLVPICRCMKAGFAVENGTVCRCPSGTTFKANOGDEACTHCPINSRTTSEGA 300
Qy 301 TNCVCRNGYYRADLPLDMPCTTIPSPAPQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Db 301 TNCVCRNGYYRADLPLDMPCTTIPSPAPQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Qy 361 ICKSCGSGRGACTRCGDNVQVAPROUGTEPRIYISDLAHTQYTFEIQAVNGVTDOSPP 420
Db 361 ICKSCGSGRGACTRCGDNVQVAPROUGTEPRIYISDLAHTQYTFEIQAVNGVTDOSPP 420

Qy 421 SPQFASVNTITNQAAAPSVAIVMHSQVSRVSDITLSWSQPDQNGVILDYELQYKEKELSE 480
Db 421 SPQFASVNTITNQAAAPSVAIVMHSQVSRVSDITLSWSQPDQNGVILDYELQYKEKELSE 480
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVQVRRVAVAGRYSGKMYFQTMTEAAYQTSIQBK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVQVRRVAVAGRYSGKMYFQTMTEAAYQTSIQBK 540
Qy 541 LPLITGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Db 541 LPLITGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Qy 601 TVEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660
Db 601 TVEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660
Qy 661 EKQRDFLSEASIMGQFDHPNVHLEGVVTKTPVMITEFNGENGLDSFLRQNDGQFTV 720
Db 661 EKQRDFLSEASIMGQFDHPNVHLEGVVTKTPVMITEFNGENGLDSFLRQNDGQFTV 720
Qy 721 IQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYDFGLSRFLEDDTSDPTY 780
Db 721 IQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYDFGLSRFLEDDTSDPTY 780
Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGVIMVMEVMSYGERPYDMTQDVINAIE 840
Db 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGVIMVMEVMSYGERPYDMTQDVINAIE 840
Qy 841 QDYRLPPMDPCPSALHOLMDCWQKDRNHRPFGQIVNTLDMKMRNPNSLKAWAPLSSGI 900
Db 841 QDYRLPPMDPCPSALHOLMDCWQKDRNHRPFGQIVNTLDMKMRNPNSLKAWAPLSSGI 900
Qy 901 NLPLDRTTIPDYSFNTVDEWLEAIKMGQYKESFANAGTSPDVVVSQMMMEDILRLGVTL 960
Db 901 NLPLDRTTIPDYSFNTVDEWLEAIKMGQYKESFANAGTSPDVVVSQMMMEDILRLGVTL 960
Qy 961 AGHQKKILNSIQVMRAQMNQIOSVE 985
Db 961 AGHQKKILNSIQVMRAQMNQIOSVE 985
RESULT 2
US-10-757-262-100
; Sequence 100, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karichetti, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE OF INVENTION: 55053
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742

;; PRIOR FILING DATE: 2003-06-16
;; PRIOR APPLICATION NUMBER: US 60/488,529
;; PRIOR FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: US 60/491,156
;; PRIOR FILING DATE: 2003-07-30
;; PRIOR APPLICATION NUMBER: US 60/499,594
;; PRIOR FILING DATE: 2003-09-02
;; PRIOR APPLICATION NUMBER: US 60/506,332
;; PRIOR FILING DATE: 2003-09-26
;; NUMBER OF SEQ ID NOS: 136
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 100
;; LENGTH: 1055
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-757-262-100

Query Match 99.9%; Score 5181; DB 17; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MALRRLLGAALLLLPLLAAVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60

Qy 61 VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120
Db 61 VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120

Qy 121 DSATKTFPNMKNWVVKVDTIAADESFQVLDGRVWVKINTEVRSFQVSRSGFYLAQD 180
Db 121 DSATKTFPNMKNWVVKVDTIAADESFQVLDGRVWVKINTEVRSFQVSRSGFYLAQD 180

Qy 181 YGGCMSLIAVRFYRKCPIRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db 181 YGGCMSLIAVRFYRKCPIRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

Qy 241 CNGDGEVLPIGRMCWKAGFEAVENGTVCRGCPGGTTFKANGQDPACTHCPINSRTTSEGA 300
Db 241 CNGDGEVLPIGRMCWKAGFEAVENGTVCRGCPGGTTFKANGQDPACTHCPINSRTTSEGA 300

Qy 301 TNCVCRNGYRADLDPDLMPCITTPSAPOAVISSNETSLMLEWTPPRDGGREDLYVNI 360
Db 301 TNCVCRNGYRADLDPDLMPCITTPSAPOAVISSNETSLMLEWTPPRDGGREDLYVNI 360

Qy 361 ICKSCGSGRGACTCGDNVQVAPQLGTEPRIYISDLLAHTQVTFEIQAVNGVTDQSPF 420
Db 361 ICKSCGSGRGACTCGDNVQVAPQLGTEPRIYISDLLAHTQVTFEIQAVNGVTDQSPF 420

Qy 421 SPQFASVNIITNQAPSAVSIHQVSRVSDITLSWSQDPQNGVILDYELQYYEKELSE 480
Db 421 SPQFASVNIITNQAPSAVSIHQVSRVSDITLSWSQDPQNGVILDYELQYYEKELSE 480

Qy 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEYQTSIQEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEYQTSIQEK 540

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Db 541 LPLIIGSSAAGLVFLIAVWVAIVCNRRGPERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600

Qy 601 TYEDPNAEVRFAKEIDISCVKIEQVIGAGEFGVCSGHLKLPKREIFVAIKLKSQYT 660
Db 601 TYEDPNAEVRFAKEIDISCVKIEQVIGAGEFGVCSGHLKLPKREIFVAIKLKSQYT 660

Qy 661 EKQRDFLSEASIMGQFDHPNVIHLEGVYKSTPVMIIITEPMENGSLDSFLRQNDGQFTV 720
Db 661 EKQRDFLSEASIMGQFDHPNVIHLEGVYKSTPVMIIITEPMENGSLDSFLRQNDGQFTV 720

Qy 721 IQLVGLMRGTAAGMKYLADNMVYHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780
Db 721 IQLVGLMRGTAAGMKYLADNMVYHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780

RESULT 3
US-10-768-158-8
; Sequence 8, Application US/10768158
; Publication No. US20040204359A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliashof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNONNIM
; CURRENT APPLICATION NUMBER: US/10768,158
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 8
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-768-158-8

Query Match 99.9%; Score 5181; DB 17; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRLLGAALLLLPLLAAVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60
Db 1 MALRRLLGAALLLLPLLAAVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60

Qy 61 VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120
Db 61 VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120

Qy 121 DSATKTFPNMKNWVVKVDTIAADESFQVLDGRVWVKINTEVRSFQVSRSGFYLAQD 180
Db 121 DSATKTFPNMKNWVVKVDTIAADESFQVLDGRVWVKINTEVRSFQVSRSGFYLAQD 180

Qy 181 YGGCMSLIAVRFYRKCPIRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db 181 YGGCMSLIAVRFYRKCPIRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

Qy 241 CNGDGEVLPIGRMCWKAGFEAVENGTVCRGCPGGTTFKANGQDPACTHCPINSRTTSEGA 300

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Db 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCGPSGTFKANQGDCACTHCPINSRTTSEGA 300
Qy 301 TNCVCRNGYRADLPLDMFCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Db 301 TNCVCRNGYRADLPLDMFCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Qy 361 CKSCGSGRACRCGDNVQAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTQSPF 420
Db 361 CKSCGSGRACRCGDNVQAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTQSPF 420
Qy 421 SPQFASVNIITNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKELSE 480
Db 421 SPQFASVNIITNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKELSE 480
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Qy 541 LPLIGSSAAGLVFLIAVVIACNRRGRFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Db 541 LPLIGSSAAGLVFLIAVVIACNRRGRFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLKSXT 660
Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLKSXT 660
Qy 661 EKQRDFLSEASIMGQFDPHNVHLEGVVTKSTPVMITTEPMENGSLDSFLRQNDGQTV 720
Db 661 EKQRDFLSEASIMGQFDPHNVHLEGVVTKSTPVMITTEPMENGSLDSFLRQNDGQTV 720
Qy 721 IOLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPY 780
Db 721 IOLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPY 780
Qy 781 TSALGGKPIRWTAPEALQYRKFTSASDVMSYIGVMEVMSYGERPYMDMTNQDVINAIE 840
Db 781 TSALGGKPIRWTAPEALQYRKFTSASDVMSYIGVMEVMSYGERPYMDMTNQDVINAIE 840
Qy 841 QDYRLPPMDCPALHQLMDCWKQDRNHRPKFGQIVNTLDKMRNPSLKAMAPLSSGI 900
Db 841 QDYRLPPMDCPALHQLMDCWKQDRNHRPKFGQIVNTLDKMRNPSLKAMAPLSSGI 900
Qy 901 NPLLDRTIPDYTSFNTVDEWLEAIKMGYKESFANAGFTSFVVSQMMEDILRLGVTL 960
Db 901 NPLLDRTIPDYTSFNTVDEWLEAIKMGYKESFANAGFTSFVVSQMMEDILRLGVTL 960
Qy 961 AGHQKKILNSIQVMAQNMNQISVE 985
Db 961 AGHQKKILNSIQVMAQNMNQISVE 985
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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 987
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-1193
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Query Match          99.7%; Score 5171.5; DB 14; Length 987;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 984; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
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Db 1 MALRLRGAALLLLPLAAVEETLMDSTTATABELGMVHPHPPSGHEVSGVDENMNTIRYQ 60
Qy 61 VCNVFESSQNNWLRTKFIIRRGGAHRHIVEMKESVDRDCSSIPSPVPSCKETENLYYEADF 120
Db 61 VCNVFESSQNNWLRTKFIIRRGGAHRHIVEMKESVDRDCSSIPSPVPSCKETENLYYEADF 120
Qy 121 DSATKTFPNMNPWVKVDTIAADESFQVDLGGRVKMKINTEVRSFGVSRGFIAPQD 180
Db 121 DSATKTFPNMNPWVKVDTIAADESFQVDLGGRVKMKINTEVRSFGVSRGFIAPQD 180
Qy 181 YGCMSSLIARVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Db 181 YGCMSSLIARVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240
Qy 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCGPSGTFKANQGDCACTHCPINSRTTSEGA 300
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Qy 301 TNCVCRNGYRADLPLDMFCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Db 301 TNCVCRNGYRADLPLDMFCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360
Qy 361 CKSCGSGRACRCGDNVQAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTQSPF 420
Db 361 CKSCGSGRACRCGDNVQAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTQSPF 420
Qy 421 SPQFASVNIITNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKELSE 480
Db 421 SPQFASVNIITNOAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKELSE 480
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Db 481 YNATAIKSPNTVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540
Qy 541 LPLIGSSAAGLVFLIAVVIACNRRGRFERADSEYTDKLOHYTSGHMTPGMKIYIDP 599
Db 541 LPLIGSSAAGLVFLIAVVIACNRRGRFERADSEYTDKLOHYTSGHMTPGMKIYIDP 600
Qy 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLKSXT 659
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RESULT 4
US-10-295-027-1193
; Sequence 1193, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
```

Db 601 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGY 660
Qy 660 TEKORRDLSEASIMGOFDHPNVHLHGVVTKSTPVMIIITEFWENGSLDSFLRQNDQOFT 719
Db 661 TEKORRDLSEASIMGOFDHPNVHLHGVVTKSTPVMIIITEFWENGSLDSFLRQNDQOFT 720
Qy 720 VIQLVGMRLGIAAGMKYLAADMVYVHRDLAARNILVNSNLVCKVSDFLSRLFLEDDTSDDPT 779
Db 721 VIQLVGMRLGIAAGMKYLAADMVYVHRDLAARNILVNSNLVCKVSDFLSRLFLEDDTSDDPT 780
Qy 780 YTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAI 839
Db 781 YTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAI 840
Qy 840 EODYRLPPPPDCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAWAPLSSG 899
Db 841 EODYRLPPPPDCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAWAPLSSG 900
Qy 900 INPLLDRTIPDYTSFNTVDEWLEAIKWGYKESFANAGFTSFVVVSQMMEDIILRLGVT 959
Db 901 INPLLDRTIPDYTSFNTVDEWLEAIKWGYKESFANAGFTSFVVVSQMMEDIILRVGLT 960
Qy 960 LAGHOKKILNSIQVMRAQMNQIQSVEV 986
Db 961 LAGHOKKILNSIQVMRAQMNQIQSVEV 987

RESULT 5

US-10-029-020-62
; Sequence 62, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 995
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-029-020-62

Query Match 96.3%; Score 4993.5; DB 15; Length 995;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;
Qy 10 LLLPLLAAREETLMDSTATAELGMMVHPSPGEEVSGYDENNNNTIRTYQVCNVPSSQ 69
Db 18 LALLPLLAAREETLMDSTATAELGMMVHPSPGEEVSGYDENNNNTIRTYQVCNVPSSQ 77
Qy 70 NNWLRTKFIIRRRGAHRIHVEMKFSVRDCSSIPSPVPGSKCTFNLYYYEADPDSATKTFPN 129

Db 78 NNWLRTKFIIRRRGAHRIHVEMKFSVRDCSSIPSPVPGSKCTFNLYYYEADPDSATKTFPN 137
Qy 130 WMENPMWVKVDITIAADESFSQVDLGGVRVMKINTEVRGPGVSRSGFYLAQDYGGCMSLIA 189
Db 138 WMENPMWVKVDITIAADESFSQVDLGGVRVMKINTEVRGPGVSRSGFYLAQDYGGCMSLIA 197
Qy 190 VRVYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
Db 198 VRVYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257
Qy 250 PIGRCMCKAGFEAVENGTVCRGCPSTGTFKANOQDEACTHCPINSRTTSEGATNCVCNCGY 309
Db 258 PIGRCMCKAGFEAVENGTVCRGCPSTGTFKANOQDEACTHCPINSRTTSEGATNCVCNCGY 317
Qy 310 YRADLPLDMPCPTTIPSAPOAVISSVNETSLMLEWTTPPRDSGGREDLVYNIICKSCSGSR 369
Db 318 YRADLPLDMPCPTTIPSAPOAVISSVNETSLMLEWTTPPRDSGGREDLVYNIICKSCSGSR 377
Qy 370 GACTRCGDNVQYAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 429
Db 378 GACTRCGDNVQYAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 437
Qy 430 TTNQAAPSAVSIHQVSRVTVDISITLSWSQDPQNGVILDYELQYKELSEYNATAKSP 489
Db 438 TTNQAAPSAVSIHQVSRVTVDISITLSWSQDPQNGVILDYELQYKELSEYNATAKSP 497
Qy 490 TTNVTVOGLKAGAIYVFOEARTVAGYGRYSGKMYFOTMTEAEVQTSIQSKLPLIGSSA 549
Db 498 TTNVTVOGLKAGAIYVFOEARTVAGYGRYSGKMYFOTMTEAEVQTSIQSKLPLIGSSA 557
Qy 550 AGLVFLIAVVVIAIVCN-RRGERADSEYTDKLQHYTSGHMTPGMKIYIDPFTYEDPNEA 608
Db 558 AGLVFLIAVVVIAIVCN-RRGERADSEYTDKLQHYTSGHMTPGMKIYIDPFTYEDPNEA 617
Qy 609 VRBFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 668
Db 618 VRBFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 677
Qy 669 SEASIMGQDPHPNVHLHGVVTKSTPVMIIITEFWENGSLDSFLRQNDQOFTVIOLVGMLR 728
Db 678 SEASIMGQDPHPNVHLHGVVTKSTPVMIIITEFWENGSLDSFLRQNDQOFTVIOLVGMLR 737
Qy 729 GIAAGMKYLAADMVYVHRDLAARNILVNSNLVCKVSDFLSRLFLEDDTSDDPTYSALGKI 788
Db 738 GIAAGMKYLAADMVYVHRDLAARNILVNSNLVCKVSDFLSRLFLEDDTSDDPTYSALGKI 797
Qy 789 PIWTAPEAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAEQDYRLPPP 848
Db 798 PIWTAPEAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAEQDYRLPPP 857
Qy 849 MDCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINLPLDRT 908
Db 858 MDCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINLPLDRT 917
Qy 909 IPDYTSFNTVDEWLEAIKWGYKESFANAGFTSFVVVSQMMEDIILRLGVTLAGHOKKIL 968
Db 918 IPDYTSFNTVDEWLEAIKWGYKESFANAGFTSFVVVSQMMEDIILRLGVTLAGHOKKIL 977
Qy 969 NSIQVMRAQMNQIQSVEV 986
Db 978 NSIQVMRAQMNQIQSVEV 995

RESULT 6

US-10-029-020-60
; Sequence 60, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020

Db 673 ERQRDFLSEASINGQFDHPNIRLEGVTKSRPVMILTFEMENCALDSFLRLNDGQFTV 732
Qy 721 IQLVGLRGTAAGKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 780
Db 733 IQLVGLRGTAAGKYLSEMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 792
Qy 781 TSALGGKIPIRWTAPAEIAQYRKFTSASDVMSYGVVMEVMSYGERPYWDMTNOQDVINAIE 840
Db 793 TSSUGGKIPIRWTAPAEIAQYRKFTSASDVMSYGVVMEVMSYGERPYWDMTNOQDVINAIE 852
Qy 841 QDYRLPPMPCPSALHQLMDCWKQDRNHRPKFCQIVNTLDKMRNPSLKAMAPLSSGI 900
Db 853 QDYRLPPMPCPTALHQLMDCWDRNLRPKFSQIVNTLDKLRNAASLKVIASAQSGM 912
Qy 901 NPLPDDTIDYTSFNTVDWLEAIKMGQYKESFANAGFTSFVDSVMMEDILRLGVTL 960
Db 913 SQPLDRTVPDYTFVTGVDLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972
Qy 961 AGHOKKILNSTQVMRAQMNQIQSVEV 986
Db 973 AGHOKKILNSTQVMRAQMNQIQSVEV 998

RESULT 9

US-10-354-358-4
; Sequence 4, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-ying
; APPLICANT: Leeson, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 5235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MF102-020P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/386,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 998

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-4
Query Match 70.6%; Score 3661.5; DB 14; Length 998;
Best Local Similarity 70.2%; Pred. No. 8e-233;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;
Qy 10 LLLPILL-----AAVEETLMDSTTATAEIAGWVHPSPSGHEEYGVYDENNTTIRTYQCN 63
Db 23 LLLPILLPAGCALTEETLMDTKWTSELAMTSHPEGWEYGVYDENNTTIRTYQCN 82
Qy 64 VFESSQNNWLRTKFIERRGAHRTHVEMKFSVRCCSIPSPVSGCKETFNLYYYEADPDSA 123
Db 83 VRESSQNNWLRTGFIWRDVORVYVELKFTVRDNCISIPNIPGCKETFNLYYYEADSDVA 142
Qy 124 TKTFPNMNMENPWKVTITAADESFSQVDLGRVYKINTEVRSFGPVSRSGFYLAQDYG 183
Db 143 SASSPFWMENPYKVDITAPDESFSRLDAG---RVNTKVRSPGLSKAGFYLAQDGA 198
Qy 184 CMSLIARVYRKCPLIQNGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKLYCNG 243
Db 199 CMSLISVRAFYKFCASTTAGFALPETLTGAETPSLVIAEPTCIPNAVEVSVPLKLYCNG 258
Qy 244 DGEWLVPIGRCMCKAGFEAVENGTVCRGCPSGTFKANQGDCACTHCPINRSTTSEGATNC 303
Db 259 DGEWVPVGNACTCATGHEPAKESQCRPCDPSYKAKQSGECPCLPCPPNSRTTSPAASIC 318
Qy 304 VCRNGYVRADLDPLDMPCTTIPSAQAVISSVNNETSLMLEWTPPRDSGGREDLVYNIICK 363
Db 319 TCHNFRADSDSADSACTTVPSPRGVISNNETSLILEWSEPRDLGVDRDLVYNIICK 378
Qy 364 SC--GSGRGACTRCGNVQYAPROLGLTEPRYIISLLAHTQYTFEILQAVNGVTDQSPFS 421
Db 379 KCHGAGGASACRCDNNEFVPRQLGSEPRVHTSHLLAHTRTFEVQAVNGVSGKSLP 438
Qy 422 POPASVNITTNQAAPSASVIMHOVSRVTDSITLSWSQDOPNGVILDYELQYKEKELSEY 481
Db 439 PRYAANVITTNQAAPSEVPTLRHLSSGSSLTLSWAPPEPENGVLIDYEMKYFEK--SEG 496
Qy 482 NATAKSPNTVTVQGLKAGAIYVQVARTVAGYRGYSGMYFQMTWE-AEYQTSIQEK 540
Db 497 IASTVTSSQMSVQLDGLRDARYVQVARTVAGYQYSRPAEFETTSERGSQAQQLQEQ 556
Qy 541 LPLIGSSAGLFLAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Db 557 LPLIVGSATAGLVFVAVVIAIVCNRRGSDSEYTKLOQY----IAPGMKYIDPF 612
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLSGYT 660
Db 613 TYEDPNEAVREFAKEIDVSCVKEEVIGAGEFGEVCRGLKQPGREVFVAIKTKVGYT 672
Qy 661 EKQRDFLSEASINGQFDHPNIRLEGVTKSRPVMILTFEMENGSLDPSFLRNDGQFTV 720
Db 673 ERQRDFLSEASINGQFDHPNIRLEGVTKSRPVMILTFEMENCALDSFLRLNDGQFTV 732
Qy 721 IQLVGLRGTAAGKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 780
Db 733 IQLVGLRGTAAGKYLSEMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 792
Qy 781 TSALGGKIPIRWTAPAEIAQYRKFTSASDVMSYGVVMEVMSYGERPYWDMTNOQDVINAIE 840
Db 793 TSSUGGKIPIRWTAPAEIAQYRKFTSASDVMSYGVVMEVMSYGERPYWDMTNOQDVINAIE 852
Qy 841 QDYRLPPMPCPSALHQLMDCWKQDRNHRPKFCQIVNTLDKMRNPSLKAMAPLSSGI 900
Db 853 QDYRLPPMPCPTALHQLMDCWDRNLRPKFSQIVNTLDKLRNAASLKVIASAQSGM 912
Qy 901 NPLPDDTIDYTSFNTVDWLEAIKMGQYKESFANAGFTSFVDSVMMEDILRLGVTL 960
Db 913 SQPLDRTVPDYTFVTGVDLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972
Qy 961 AGHOKKILNSTQVMRAQMNQIQSVEV 986

304 VCRNGYRADLDPLDMPCTTIPSAQAVISSNETSLMELWTPPRDSGGREDLVNICK 363
328 TCHNFYRADSDSADACTIVSPRGVJSNNNETSLILESEPRDLGVRDLDLVNICK 387
364 SC--GSGRGACTCGDNVQYAPRQLGLTEPRYIYISDLAHTQYTFEIOAVNGVTDQSPFS 421
388 KCHGAGGASACSRCDNVEFVRQLGLSEPRVHTSHLLAHTYTFEIOAVNGVSKSLP 447
422 POFASVNIITNOAAPSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELSEY 481
448 PRYAANIITNOAAPSEVPTLHLHSSGSSLTLSWAPPENGVILDELYEYKELSEY 505
482 NATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGVGRYSGRMVFTQWTE-AEYQTSIOEK 540
506 IASTVTSQNSVQLDGLRPDARYVQVRAARTVAGVGRYSGRMVFTQWTE-AEYQTSIOEK 565
541 LPLITGSSAAGLVLIIVVIAVNCNRRGFERADSEYTDKQHTYSGHMTGPKMIYIDPF 600
566 LPLIVGSATAGLVFVAVVIAVCLRKQRHGSDEYTEKLQY----IAPGMKVIYIDPF 621
601 TYEDDNEAVREPAKIDISCVKIEOVIGAGFGEVCSCHLKLPGKREIFVIAIKLKSQYT 660
622 TYEDDNEAVREPAKIDISCVKIEOVIGAGFGEVCSCHLKLPGKREIFVIAIKLKSQYT 681
661 EKQRDFLSEASIMQFDPHPNVHLEGVVTKSTPVIITPFWNGSLDSFLRQNDGQTV 720
682 ERQRDFLSEASIMQFDPHPNIIRLEGVVTKSRPVIITPFWNGSLDSFLRQNDGQTV 741
721 IOLVGLRGIAAGMKYLDAMVYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 780
742 IOLVGLRGIAAGMKYLDAMVYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPT 801
781 TSALGCKIPIRWTAPEALQYKFTSASDVWSYGVVMEVMSYGERPYWDMTNDVINAIE 840
802 TSSLGCKIPIRWTAPEALQYKFTSASDVWSYGVVMEVMSYGERPYWDMTNDVINAIE 861
841 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFQIVNTLDKMRNPNLSKAMAPLSSGI 900
862 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFQIVNTLDKMRNPNLSKAMAPLSSGI 921
901 NLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSVMSOMMEDILRLGVTL 960
922 SQPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDSVMSOMMEDILRLGVTL 981
961 AGHOKILNSIQVMRAQNNQIQSVEV 986
982 AGHOKILNSIQVMRAQNNQIQSVEV 1007

RESULT 12

US-10-187-958-1
; Sequence 1, Application US/10187958
; Publication No. US20030170865A1
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; KITAGAWA, KOICHIRO
; OHNO, HIROYUKI
; UENO, TOSHIO
; TITLE OF INVENTION: A No. US20030170865A1el Polypeptide of Protein p140
; and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10187,958
; FILING DATE: 03-Jul-2002
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,340
; FILING DATE: 26-APR-2000
; APPLICATION NUMBER: 09/192,435
; FILING DATE: 08-JAN-1998
; APPLICATION NUMBER: 08/571,785
; FILING DATE: 13-DEC-1995
; APPLICATION NUMBER: 08/348,143
; FILING DATE: 23-NOV-1994
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-187-958-1

Query Match 69.5%; Score 3603.5; DB 14; Length 993;
Best Local Similarity 68.5%; Pred. No. 5.4e-229;
Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

QY 17 AAVEETLMDSTATA-----ELGMVHPSPSGWEVSGYSDMMTIRTY 59
DB 11 AAARAATAATNSLSILVRPTSEGRIDSEFVELAWTSHPSGWEVSAIDSAMPIRTY 70
QY 60 QVCNVFESSQNNWLRTKFIIRRGAIHIVEMKFSVRDCSSIPSPGCKETENLYVEAD 119
DB 71 QVCNVRESSQNNWLRTGFIIRREVQVYVELKFTVRDCNSINIPGCKETENLYVEAD 130
QY 120 FDSATKTFPNWENFWKVDTIAADESFQVDLGRVMKINTEVRSFGVSRSGYLAFQ 179
DB 131 SDVASASSPFWMENPVYKVDTIAPDESFSRLDAG---RVNTKVRSFGPLSKAGFLAFQ 186
QY 180 DYGGGMSLIAVRFYRKCPRIIQNGAIFOETLSGAESTLSVAARGSCIANAEVDVPIKL 239
DB 187 DQACMSLISVRAFYKCASTAGTALPPELITGAEPTLSLVATPGTCLANAEVSVPLKL 246
QY 240 YCNGDEMLVPIGRCMCKAGFEAVNGTVCRGCPSTGTFKANGQDBACTHCPINSRTTSEG 299
DB 247 YCNGDEWVVPVGACTCATGHEPAKETQCRACPPGSKAKQGEGLPCPCPNSTTSPA 306
QY 300 ATNCVCRNGYRADLDPLDMPCTTIPSAQAVISSNETSLMELWTPPRDSGGREDLVN 359
DB 307 ASICTCHNFRADSDTADSACTTVPSPRGVSNVNETSLILEWSEPRDLGGRRDLYN 366
QY 360 IICKSCGSGRGA-----CTRCGDNVQYAPRQLGLTEPRYIYISDLAHTQYTFEIOAVNGV 414
DB 367 VICCKCRGSSGAGGATCSRCDDNVEFVRQLGLSEPRVHTSHLLAHTYTFEIOAVNGV 426
QY 415 TDQSPFSQPFASVNIITNOAAPSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELSEY 474
DB 427 SGKSLPFPYAAVNIITNOAAPSIMQVSRVDSITLSWSQDPQNGVILDELYEYKELSEY 486
QY 475 EKELSEYNATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGVGRYSGRMVFTQWTE-AEY 533
DB 487 EK--SKGIASVTSSQKNSVQLDGLQPDARYVQVRAARTVAGVGRYSGRMVFTQWTE-AEY 544

[illegible]

RESULT 13

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US-10-408-765A-2942
; Sequence 2942, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC
; TITLE OF INVENTION: IDENTIFIED IN THE MIT
; FILE REFERENCES: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2942
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2942

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	Query Match	69.3%	Score 3594.5	DB 16	Length 896
	Best Local Similarity	73.5%	Pred. No. 1.9e-228		
	Matches 655	Conservative 123	Mismatches 112	Indels 1	Gaps 1
Qy	90	MKFSVRDCSSITPSVPGSKCTFNILYYEADPDSATKTFPNMNPWKVDITIAADESFQ	149		
Db	1	MRFTVRDCSSLPNVPGSKCTFNILYYETTSVIATKGSAPFWESEAPYLKVDITIAADESFQ	60		
Qy	150	VDLGGVRWVKINTEVRSFGPVSFGYLAFODYGGCMLIAVRVYRFRKCPRIIIONGAIFQE	209		
Db	61	VDPGRLMKYNTVRSFGPLTRNGFYLAFODYGACMSLLSVRVVFKKCPISVQNFVPE	120		
Qy	210	TLGAESTSLVAARGSCIANAEVDVPIKLYCNGDGBWLVDPIGRCMCKAGFEAVENGTVTC	269		
Db	121	TMTGAESTSLVARGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGVEP-ENSVAC	179		

RESULT 14

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US-10-029-020-61
; Sequence 61, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358

```

	Query Match	58.8%; Score 3053; DB 10; Length 991;
	Best Local Similarity	58.8%; Pred. No. 1.2e-192;
	Matches 573; Conservative	165; Mismatches 224; Indels 12; Gaps 9
Qy	6 LGAALLLLPLAAVEETLMDSTTATAELGHWVHPSPGWEVSVDYDENMMTIITYQVCNVF	65
Dd	22 LCAALRTLASPSNEVNLLDSRTVMGLGWIAFPKNGWEEIGEVSDENYAPIHTYQVCVKM	81
Qy	66 ESSQNWLRTKFIRRRGAHRIVHEMKFSVRDCSSIPSVPGCKEFTNLNYYEADPDSATK	125
Dd	82 EQNQNNLLTSWIENEGASRIFELKRLTKDNCNSLPFGGLGTKEFTNMIFYESDDQNGR	140
Qy	126 TFPNNMENPWKVDTITAADESFQVDLGGRVKMINTFEVRSFGPVSRSGFYLLAFQDYGC	185

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Db 141 ---NIKENQYIKIDTIAADESFTDLGDRVMKLNTEVRDVGPLSKGKGYLAFOVDGACI 197
Qy 186 SLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDG 245
Db 198 ALVSRVYRKCPSPVHLAVFPDTITIGADSSQLLEVSGSCV-NHSTVDEPPRKHCSAEG 256
Qy 246 EWLPIGRCMKCAGFEAVENGTCRCGPGSTGTFKANQDEACTHCPINSRTTSEGATNCVC 305
Db 257 EWLPIGRCMKCAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVC 314
Qy 306 RNGYTRADLDPLDMPCTTIISAPQAVISSVNETSLMLEWTPPRDSGGREDLVNIIKSC 365
Db 315 EKDYFRRESPPPTWACTRPPSAPRNAISNVNETSVFLWIPADTGGRKDVSVYIACKKC 374
Qy 366 GSGRGACTRCGDNQVAPQRLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSQPEA 425
Db 375 NSHAGVCECGHVRYPQSGGLKNTSMVMVDLHAHTYFIEIENVNGVSDLSGCAQYV 434
Qy 426 SVNITTNQAAPSAYSIMHQSRTVDSITLSWSQDPNGVILDYELQYKEKELSEYNATA 485
Db 435 SVNITTNQAAPSPVTVNKKGIKANSISLSWQEDPRNGIILEYIKHFEKD-QETSYTI 493
Qy 486 IKSTPTNTVOGLKAGAIYFQVRARTVAGRYSGKMYFQTMTEABYQTSIQEKLPLII 545
Db 494 IKSKETTITAEGLKPAVYFQIRARTAAGYGVFSRRPEFET-TPVPAASSDQSQIPVIA 552
Qy 546 GSSAAGVFLJAVVVAIACNRRGFERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYED 604
Db 553 VSVTVGVILLAVVIGVLLSGRCYSAKQDPEEEKWHFHNGHILKPGVRTYIDPHTYED 612
Qy 605 PNEAVRFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPKREIFVAIKTLKSGYTEKOR 664
Db 613 PNQAVHFAKEIEASCITIERVIGAGFGEVCSGRLKLPKRELPAIKTLKVGYTEKOR 672
Qy 665 RDLSEASIMQDPHPNVHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTVQLV 724
Db 673 RDLSEASIMQDPHPNVHLEGVYTKSTPMIITEFMENGSLDTFLKQNDGQFTVQLV 732
Qy 725 GMLRGIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYSAL 784
Db 733 GMLRGISAGMKYLDGMYVHRDLAARNILVNSNLVCKVSDPGLSRVLEDD-PEAYTTR- 790
Qy 785 GGIPIRTAPEAIOYRKFTSASDWSYGIWMVEVMSYGERPYWDMTNQDVINAIEQDYR 844
Db 791 GGIPIRTAPEAIAFRKFTSASDWSYGIWMVEVMSYGERPYWDMTNQDVIKAVEGYR 850
Qy 845 LPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPL 904
Db 851 LPSMDCPSALYQLMDCQKERNRSPKFDIIVNMLDKLIRNPSLTLVNASCRVSNLL 910
Qy 905 LDRTPDYTSFNTVDEWLEALIKMGYKESPANAGFTSFDVVSOMMEDILRLGVTLAGHQ 964
Db 911 AEHSPLASGATRYGVEWLEALIKMGYKESIFEMNGTSSMDAVAQVTLDDRRLGVTLAGHQ 970
Qy 965 KKIILNSIQVMRAQM 978
Db 971 KKIILNSIQVMKVL 984
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RESULT 16

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US-10-412-277-7
; Sequence 7, Application US/10412277
; Publication No. US20030175791A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067DIV
; CURRENT APPLICATION NUMBER: US/10/412,277
; CURRENT FILING DATE: 2003-04-14
; NUMBER OF SEQ ID NOS: 8
```

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; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 7
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; LENGTH: 953
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; TYPE: PRT
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; ORGANISM: Human
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US-10-412-277-7
```

```
Query Match 58.8%; Score 3048; DB 14; Length 953;
Best Local Similarity 59.2%; Pred. No. 2,4e-192;
Matches 568; Conservative 164; Mismatches 216; Indels 12; Gaps 9;
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Qy 20 EETLMDSSTTAELGHWVHPSPSWEEVSGYDENWNTIRTYQVCNVFESSQNNMLRTFPIR 79
Db 3 EVNLLDSRTVMGLDGIAPFKNGWEEIGEDENYAPIHTYQVCKWBEQNNMLLTWSIS 62
Qy 80 RRGARHIVBMKFSVRDCSSIPSPGSKETENLYXYEADFDSATKTFPNMNMENPMVKVD 139
Db 63 NEGASRIFILKLTFLRDCNSLPGGLGTCKETFNMYFESDDQNGR----NIKENQYIKID 118
Qy 140 TIAADESFQSDVLGGRVMKINTEVRSGFVLAFOYDYGCMSLIAVRVYRKCPR 199
Db 119 TIAADESFTELDLDGRVMKLNTEVRDVGPLSKGKGYLAFOVDGACIALVSRVYRKCP 178
Qy 200 IIONGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGWLVPIGRCMKCAG 259
Db 179 VVRHLAVFPDTITIGADSSQLLEVSGSCV-NHSTVDEPPRKHCSAEGWLVPIGRCMKCAG 237
Qy 260 FEAVENGTCRCGPGSTGTFKANQDEACTHCPINSRTTSEGATNCVCNRYRDLPLDM 319
Db 238 YEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDIFRRESDP 295
Qy 320 PCTTIPSAPQAVISSVNETSLMLEWTPPRDSGGREDLVNIIKSCSGRGACTRCGDNV 379
Db 296 ACTRPPSAPRNAISNVNETSVFLWIPADTGGRKDVSVYIACKKCNHAGVCECGHV 355
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSQPAFASVNTTNQAASAV 439
Db 356 RYLPROSGLKNTSMVMVDLHAHTYFIEIENVNGVSDLSGPAQYVSVNTTNQAASPV 415
Qy 440 SIMHQSRTVDSITLSWSQDPNGVILDYELQYKEKELSEYNATAIKSPNTNTVVOGLK 499
Db 416 TNVKGKIAKNSISLSWQEDPRNGIILEYIKHFEKD-QETSYTIKSKETTITAEGLK 474
Qy 500 AGAIYFQVRARTVAGRYSGKMYFQTMTEABYQTSIQEKLPLIIIGSSAAGLVFLIAV 559
Db 475 PASVYVFOIRARTAAGYGVFSRRPEFET-TPVPAASSDQSQIPVIAVSVTVGVILLAVI 533
Qy 560 VIAICNRRGFERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYEDNEAVRFAKEIDI 618
Db 534 GVLLSGRCYSAKQDPEEEKWHFHNGHILKPGVRTYIDPHTYEDPNQAVHFAKEIEA 593
Qy 619 SCVKIEQVIGAGFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDFLSEASIMQFD 678
Db 594 SCITIERVIGAGFGEVCSGRLKLPKRELPAIKTLKVGYTEKQRDFLGEASIMQFD 653
Qy 679 HPNVHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTVQLVGMRLGIAAGMKYLA 738
Db 654 HPNIIHLEGVYTKSPVMIITEFMENGSLDTFLKQNDGQFTVQLVGMRLGISAGMKYLS 713
Qy 739 DMNVVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALCGKPIRTAPEAI 798
Db 714 DMGVHRDLAARNILVNSNLVCKVSDPGLSRVLEDD-PEAYTTR-GGKPIRTAPEAI 771
Qy 799 QYRKFTSASDWSYGIWMVEVMSYGERPYWDMTNQDVINAIEQDYRILPPMDCPSALHQL 858
Db 772 AFRKFTSASDWSYGIWMVEVMSYGERPYWDMTNQDVIKAVEGYRLPSMDCPSALYQL 831
Qy 859 MLDQWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTIPDYTSFNTV 918
Db 832 MLDQWQKERNRSPKFDIIVNMLDKLIRNPSLTLVNASCRVSNLLAEHSPGLSGAYRSV 891
Qy 919 DEWLEALIKMGYKESPANAGFTSFDVVSOMMEDILRLGVTLAGHQKILNSIQVMRAQM 978
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Db 892 GEMLEAKMGKRYTEIFWENGYSMDAVAQVTLLEDRRLGLVTLVGHQKIMNSLOEKVQL 951

RESULT 17

US-10-723-860-597
; Sequence 597, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 597
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-597

Query Match 58.7%; Score 3045; DB 17; Length 986;

Best Local Similarity 59.3%; Pred No. 3.9e-192; Indels 40; Gaps 12;
Matches 580; Conservative 146; Mismatches 212;

QY 18 AVEETLMDSTATAELGMMVHP-PSGEEVSGYDENMNTIRTYQCVNVFSSQNNLRITK 76
Db 28 ANEVTLLDSRSVQGLGWIAGPLEGGEVSVIMDEKNTPIRTYQCVNVFSSQNNLRITD 87
QY 77 FTRREGARHIVHEKFSVDCSSIPSPVSCKEFNLYIYEAADPSATKTFPNMENPWV 136
Db 88 WITREGARVIEIKFTLRDNCNLPVGMGTCKETFNLYIYESSDNDKERFI-----RENQFV 143
QY 137 KVDITADESFSDVLGKRVNKINTEVRSGFVSRSGFYLAFOYGGCMSLIAVRVYRK 196
Db 144 KIDITADESTQVDIGDRIMKLNTEIRDVGLSKGFLYAFQDVGVGACIALVSVRVYRK 203
QY 197 CPRIIONCAIQTSLGABSTSLVAAGCSITANAEVDVPIKLYCNGDGLWLPVIGRCMC 256
Db 204 CPLVRNLQAPDPTITGADTSSLVVRGSCVNNSEKDVV-KMYCGADGEWLPVIGNCLC 262
QY 257 KAGFEAVENGTVCRGCPSTGPKANQGBEACTHCPIINSRTTSEGATNCVCRNGYTRADLDP 316
Db 263 NAGHE--ERSGEOACKIGYKALSTDTATCKCPHSHYSWEGATCTCDRGFFRADNDA 320
QY 317 LDMPTTIPSAQVIVSNVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSG-RGACTRC 375
Db 321 ASMPCTRPSPAPLNLISNVNETSVNLEWSSPQNTGGRQDISYVNVCKKCGAGDPKCRPC 380
QY 376 GDNVOYAPROGLTEPRIYISDLIAHTQYTFEQAQVNGVTDQSPFPQFASVNIITNOAA 435
Db 381 GSGVHYTPQOGLTKTKVSTDLIAHTNYTFEIVAVNGVSKYVNPDPQSVSVTVITNOAA 440
QY 436 PSVSIHMOVSRTVDSITLSWSPQDPQNGVILDYEQYVEKSELSEYNATAIKSPPTNTTV 495
Db 441 PSSIALVQAEVTRYVALAWLEDPDRENGVILEVYKYEKQDNERSYRIVRTAAARTDI 500
QY 496 QGLKAGAIYVFOVARTVAGRYSGKQYFQTTWEABYQTSIQEKLPL-LIIGS-----547
Db 501 KGLNPLTSYFVHRAARTAGYGFSEPLEVTNT-----VPSRIIGDGANSTVL 549
QY 548 --SAAGLVFLIAVVIIVCNRR--GPERADSEVTDKLYHTSGHMTPGMKIYIDPFTYE 603
Db 550 LVSVSGSVLVLVILIAFVLSRRSKYSKAKQADEE-----KHLNQGVRTYVDPFTYE 603
QY 604 DPNEAVREFAKEIDISCVKIQVIGAGEFCGVCSEHKLKPGKREIFVAIKLSGYTEKQ 663
Db 604 DPNQAVREFAKEIDASCIEKIVGIVGFCGVCSEHKLKPGKREICVAIKLKAGYTDKQ 663

QY 664 RRDFLSEASIMQFDPHNVIIHLEGVTKSTPVMIIITFMENGSLDSFLRQNDGQFTVIOL 723
Db 664 RRDFLSEASIMQFDPHNVIIHLEGVTKSTPVMIIITFMENGSLDSFLRQNDGQFTVIOL 723
QY 724 VMLRGITAGKYLADNMYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDSDPTVYTS 783
Db 724 VMLRGITAGKYLADNMYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDSDPTVYTS 783
QY 784 LGGKIPRTWAPRAIOYRKETSASDVMSYGVVMEVMSYGERPYWDMTQDVINAIEODY 843
Db 784 LGGKIPRTWAPRAIOYRKETSASDVMSYGVVMEVMSYGERPYWDMTQDVINAIEODY 843
QY 844 RLPPMDPCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLP 903
Db 844 RLPPMDPCPSALHQLMDCWQKDRNRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLP 903
QY 904 LLDRTTIDYTSFNTVDENLEAIKMGQYKSFANAGTSTFSDVVSQMMEDILRLGVTLGH 963
Db 904 LLDRTTIDYTSFNTVDENLEAIKMGQYKSFANAGTSTFSDVVSQMMEDILRLGVTLGH 963
QY 964 QKKILNSIQVWRAQMNQI 981
Db 964 QKKILNSIQVWRAQMNQI 981

RESULT 18

US-09-823-187-39
; Sequence 39, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 39
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-823-187-39


```
Query Match      58.6%; Score 3038.5; DB 10; Length 993;
Best Local Similarity 59.3%; Pred. No. 1.1e-191;
Matches 573; Conservative 153; Mismatches 225; Indels 15; Gaps 8;

Qy 17 AAVEETLMDSTTATAEGLVHPPSGWEEVSGYDENMNTTIRTYQVNCVFPSSQNNWLRTK 76
Db 29 AAKEVILLDSKAQOETELEWISSPPNGWEEISGLDENYTPRTYQVQVWESNNQNLRTN 88
Qy 77 FIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTFPNMNPV 136
Db 89 WIAKSNQRIFFVELKFTLRDCNSLPGLGTCKETFNLYYYETD-----TGRNIRENQYV 144
Qy 137 KVDTIAADESFSQVDLGGVRVMKINTEVRSPGVSFGYLAFOYGGCMSLIAVRVYRK 196
Db 145 KIDTIAADESFTQDGLGERKMKLNTVEIRGIPLSKKGFLAFQDVGCIALVSVKYYKK 204
Qy 197 CPRIIONGAIFQETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGEWLVPIGRM 255
Db 205 CWSIIENLAIPDVTGSEFSSLVVRGTCVSSABEEAENSPKMHCSABGEWLVPIGKCI 264
Qy 256 CKAGFAVENGTVCRCGCPSTFKANQOGEACTHCPINSTRTTSEGATNCVCRNGYRADLD 315
Db 265 CKAGYQ--QKGDTCPCGRGFYKSSQDLQCSRCPHSPDKGSSRCDSDSYRAPSD 322
Qy 316 PLDMPTTIPSAQVAVISSVNETSLMLEWTPPRDSGGREDLVNIIICKSCSGRGACTRC 375
Db 323 PPVACTRPPSAPQNLIFNINQTTVLEWSPADNGRNDVYRILCKRCSWEQGEVCP 382
Qy 376 GDNVOYAPROLGLTEPRIYISDLAHTQYFEIOAVNGVTDQSPFPQFASVNTTNOAA 435
Db 383 GSNIGYMPQQTGLVDNVTVMDDLHANYTFEVAVNGVSDLSRQSLFAAVSITTCQAA 442
Qy 436 PSAVISIMHOVSRTVDSITLWSQDPQNGVLDYELQYKELSEYNATAIKSPNTNVTV 495
Db 443 PSQVSGVWKERVLSQELSWQEPHNGVITEIKYKQDRERYSTVTKSTGASI 502
Qy 496 QGLKAGAIYVQVARTVAGRYSGKMYFQMTAEAYQTSIQEKLPLIIGS--SAGLV 553
Db 503 NNLKPGTVVYFQIRAFTAAGYGNYSRPLDVLATLEATATAVSSBQNPVILIAVVAVAGTI 562
Qy 554 FLIAVVVIAVCNRR-GFERADSEYTKLQHYTSGHMTGPKMIYIDPFTYEDPNEAVREF 612
Db 563 ILVFMVFGPIGRHCGYSKADQGBELVPH---FKPPGKTGYIDPETYEDPNRAVHQF 619
Qy 613 AKEDIDCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYTEKORRDLSEAS 672
Db 620 AKELDASCIEKIERVIGAGEFGEVCSGRLKLPGRKRDVAIKLVKGYTEKORRDLCEAS 679
Qy 673 IMGQFDHPNVHLEGVVTKSTPVMIIITPEMNGSLDSFLRQNDGQFTVIQLVGMRLGIAA 732
Db 680 IMGQFDHPNVHLEGVVTRGKPMVIEYMEAGALDAFLRKHQDQFTVIQLVGMRLGIAA 739
Qy 733 GMKYLADNMYVHRLAARNILVNSNLVKVSDPGLSRFLDSDTDPYTSALGKPIRW 792
Db 740 GMRYLADMGVYHRLAARNILVNSNLVKVSDPGLSRVIEDD-PEAVYTTT-GGKIEPVR 797
Qy 793 TAPAIQVRFKTSASDVWSYGVIMVWESYGERPYWDMTQDYNATQDYRLPPMDCP 852
Db 798 TAPAIQVRFKTSASDVWSYGVIMVWESYGERPYWDMNQDVTKALEEGRULPAPMDCP 857
Qy 853 SALHQLMDCQKQDRNHRPFGQIVNTLDKMRNPNSLKAMAPLSSGNLFLDRTIPDY 912
Db 858 AGLHQLMDCQKQGERPKEQIVGLIDKMRNPNSLTKPLGTCSRPIPLDQNTPDF 917
Qy 913 TSFNTVDEWLEAIKQGVKESFANAGFTSFDVUSQMMEDILRLGVTLAGHQKILNSIQ 972
Db 918 TTFCSVGEWLOAIKVERYKONFTAAAGYNSLESVARMTIEDVMSLGITLVGHQKIMSSIQ 977
Qy 973 VMRAQM 978
Db 978 TMRAQM 983
```

RESULT 19
US-09-823-187-41
: Sequence 41, Application US/09823187
: Publication No. US20030096952A1
: GENERAL INFORMATION:
: APPLICANT: Burgees, Catherine
: APPLICANT: Gusev, Vladimir Y
: APPLICANT: Liu, Xiaohong
: APPLICANT: Majumder, Kumud
: APPLICANT: Padigaru, Muralidhar
: APPLICANT: Patturajan, Meera A
: APPLICANT: Shimkets, Richard A
: APPLICANT: Spaderna, Steven K
: APPLICANT: Spytek, Kimberly
: APPLICANT: Taupier, Raymond J
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 15966-745
: CURRENT APPLICATION NUMBER: US/09/823,187
: CURRENT FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/193,339
: PRIOR FILING DATE: 2000-03-30
: PRIOR APPLICATION NUMBER: 60/193,205
: PRIOR FILING DATE: 2000-03-30
: PRIOR APPLICATION NUMBER: 60/195,343
: PRIOR FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: 60/195,088
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,005
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/195,792
: PRIOR FILING DATE: 2000-04-10
: PRIOR APPLICATION NUMBER: 60/196,556
: PRIOR FILING DATE: 2000-04-11
: PRIOR APPLICATION NUMBER: 60/197,081
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: 60/197,525
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/197,087
: PRIOR FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 41:
: LENGTH: 993
: TYPE: PRT
: ORGANISM: Gallus gallus
US-09-823-187-41

Query Match 58.6%; Score 3038.5; DB 10; Length 993;
Best Local Similarity 59.3%; Pred. No. 1.1e-191;
Matches 573; Conservative 153; Mismatches 225; Indels 15; Gaps 8;

Qy 17 AAVEETLMDSTTATAEGLVHPPSGWEEVSGYDENMNTTIRTYQVNCVFPSSQNNWLRTK 76
Db 29 AAKEVILLDSKAQOETELEWISSPPNGWEEISGLDENYTPRTYQVQVWESNNQNLRTN 88
Qy 77 FIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTFPNMNPV 136
Db 89 WIAKSNQRIFFVELKFTLRDCNSLPGLGTCKETFNLYYYETD-----TGRNIRENQYV 144
Qy 137 KVDTIAADESFSQVDLGGVRVMKINTEVRSPGVSFGYLAFOYGGCMSLIAVRVYRK 196
Db 145 KIDTIAADESFTQDGLGERKMKLNTVEIRGIPLSKKGFLAFQDVGCIALVSVKYYKK 204
Qy 197 CPRIIONGAIFQETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGEWLVPIGRM 255
Db 205 CWSIIENLAIPDVTGSEFSSLVVRGTCVSSABEEAENSPKMHCSABGEWLVPIGKCI 264
Qy 256 CKAGFAVENGTVCRCGCPSTFKANQOGEACTHCPINSTRTTSEGATNCVCRNGYRADLD 315
Db 265 CKAGYQ--QKGDTCPCGRGFYKSSQDLQCSRCPHSPDKGSSRCDSDSYRAPSD 322
Qy 316 PLDMPTTIPSAQVAVISSVNETSLMLEWTPPRDSGGREDLVNIIICKSCSGRGACTRC 375
Db 323 PPVACTRPPSAPQNLIFNINQTTVLEWSPADNGRNDVYRILCKRCSWEQGEVCP 382
Qy 376 GDNVOYAPROLGLTEPRIYISDLAHTQYFEIOAVNGVTDQSPFPQFASVNTTNOAA 435
Db 383 GSNIGYMPQQTGLVDNVTVMDDLHANYTFEVAVNGVSDLSRQSLFAAVSITTCQAA 442
Qy 436 PSAVISIMHOVSRTVDSITLWSQDPQNGVLDYELQYKELSEYNATAIKSPNTNVTV 495
Db 443 PSQVSGVWKERVLSQELSWQEPHNGVITEIKYKQDRERYSTVTKSTGASI 502
Qy 496 QGLKAGAIYVQVARTVAGRYSGKMYFQMTAEAYQTSIQEKLPLIIGS--SAGLV 553
Db 503 NNLKPGTVVYFQIRAFTAAGYGNYSRPLDVLATLEATATAVSSBQNPVILIAVVAVAGTI 562
Qy 554 FLIAVVVIAVCNRR-GFERADSEYTKLQHYTSGHMTGPKMIYIDPFTYEDPNEAVREF 612
Db 563 ILVFMVFGPIGRHCGYSKADQGBELVPH---FKPPGKTGYIDPETYEDPNRAVHQF 619
Qy 613 AKEDIDCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYTEKORRDLSEAS 672
Db 620 AKELDASCIEKIERVIGAGEFGEVCSGRLKLPGRKRDVAIKLVKGYTEKORRDLCEAS 679
Qy 673 IMGQFDHPNVHLEGVVTKSTPVMIIITPEMNGSLDSFLRQNDGQFTVIQLVGMRLGIAA 732
Db 680 IMGQFDHPNVHLEGVVTRGKPMVIEYMEAGALDAFLRKHQDQFTVIQLVGMRLGIAA 739
Qy 733 GMKYLADNMYVHRLAARNILVNSNLVKVSDPGLSRFLDSDTDPYTSALGKPIRW 792
Db 740 GMRYLADMGVYHRLAARNILVNSNLVKVSDPGLSRVIEDD-PEAVYTTT-GGKIEPVR 797
Qy 793 TAPAIQVRFKTSASDVWSYGVIMVWESYGERPYWDMTQDYNATQDYRLPPMDCP 852
Db 798 TAPAIQVRFKTSASDVWSYGVIMVWESYGERPYWDMNQDVTKALEEGRULPAPMDCP 857
Qy 853 SALHQLMDCQKQDRNHRPFGQIVNTLDKMRNPNSLKAMAPLSSGNLFLDRTIPDY 912
Db 858 AGLHQLMDCQKQGERPKEQIVGLIDKMRNPNSLTKPLGTCSRPIPLDQNTPDF 917
Qy 913 TSFNTVDEWLEAIKQGVKESFANAGFTSFDVUSQMMEDILRLGVTLAGHQKILNSIQ 972
Db 918 TTFCSVGEWLOAIKVERYKONFTAAAGYNSLESVARMTIEDVMSLGITLVGHQKIMSSIQ 977
Qy 973 VMRAQM 978
Db 978 TMRAQM 983

Qy 664 RRDFLSASINGQFDHPNVHLEGVVTKSTPVMITFTFMENGLSDSLRQNDGQFTVIQL 723
Db 664 RRDFLSASINGQFDHPNVHLEGVVTKSTPVMITFTFMENGLSDSLRQNDGQFTVIQL 723
Qy 724 VGLMGLTAAAGKYLADWNYVHRDLAARNILVNSLVCKVSDPGLSRLEDDTDPYTTSA 783
Db 724 VGLMGLTAAAGKYLADWNYVHRDLAARNILVNSLVCKVSDPGLSRLEDDTDPYTTSA 783
Qy 784 LGGKIPRTAPEAIQYRKFTSASDVMSYGIVMVEVMSYGRPYWDMTQDQVINAIBQDY 843
Db 784 LGGKIPRTAPEAIQYRKFTSASDVMSYGIVMVEVMSYGRPYWDMTQDQVINAIBQDY 843
Qy 844 RLPPMDCPSALHQLMDCQKORHNRKPKFQIVNTLDKMRNPNNSKAMAPLSSGNLNP 903
Db 844 RLPPMDCPSALHQLMDCQKORHNRKPKFQIVNTLDKMRNPNNSKAMAPLSSGNLNP 903
Qy 904 LLDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLACH 963
Db 904 LLDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLACH 963
Qy 964 QKILNLSQVMAQWQNI 981
Db 964 QKILNLSQVMAQWQNI 981
Qy 962 QNKILSSQVMAQWQNI 979
Db 962 QNKILSSQVMAQWQNI 979

RESULT 21
US-10-316-124-3
; Sequence 3, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MP101-291P1EM
; CURRENT APPLICATION NUMBER: US/10316,124
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-3

Query Match 58.5%; Score 3036; DB 14; Length 1037;
Best Local Similarity 57.6%; Pred. No. 1.6e-191;
Matches 574; Conservative 165; Mismatches 223; Indels 34; Gaps 11;
Qy 6 LGAALLPLLAAYEETLMDSTTATAEIGWVHPSPGWEVSGYDENMNTIRTYQVCNVF 65
Db 46 LCAALRTLLASPSNEVLLDSRTWGLDGTAFPNAGWEEIGEVDENYAPHTYQVCNM 105
Qy 66 ESSQNNWLRTKFIIRRGAAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSATK 125
Db 106 EQNNWLLTSWISNEGASRIFELKFTLRDCNSLPGGLGTCKETFNMYFESDQNGR- 164
Qy 126 TFPNWMNPVKTUAIADSFSDVLDLGRVWKLNTVRSFPGVSRSGFYLAFOYGGCM 185
Db 165 ---NIKENQYIKIDTIAADESFTLDELGRVWKLNTVRSFPGVSRSGFYLAFOYGGACI 221
Qy 186 SLIAVRVYRKPRIIQQNGAIFQTLGABSTSLVAARGSCIANAEVDDVPILKLYCNGDG 245
Db 222 ALVSRVYRKPRIIQQNGAIFQTLGABSTSLVAARGSCIANAEVDDVPILKLYCNGDG 280
Qy 246 EWLVPICMKCAGFAEAVENGTCVCGPSGFFKANQDEACTHCPINSRTTSEGATNCVC 305
Db 281 EWLVPICMKCAGFAEAVENGTCVCGPSGFFKANQDEACTHCPINSRTTSEGATNCVC 338
Qy 306 RNVYRADLPLDMPCTTIPSAQVATSSVNETSLMLEWTPPRDSGGREDLVNIIKSC 365
Db 306 RNVYRADLPLDMPCTTIPSAQVATSSVNETSLMLEWTPPRDSGGREDLVNIIKSC 365

Db 339 EKDYFRSEDPPTMACTRPPSAPRNAISNVNYSVFLWLEIPADTGGKRVSYIACKKC 398
Qy 366 GSGRGACTRCNDVQVAPRQGLTEPRYISDLIAHTQYTFEIOAVNGVTDQSPFSPQFA 425
Db 399 NSHAGVCEEGCHVRYLPRQSLKNTSVMMVVDLLAHTNYTFEAVNGVSDLSFGARQYV 458
Qy 426 SVNITNQAAPSASVIMHVSRTVDSITLWSQDOPNGVILDYELYYEKEUSEYNATA 485
Db 459 SVNITNQAAPSASVIMHVSRTVDSITLWSQDOPNGVILDYELYYEKEUSEYNATA 517
Qy 486 IKPTNTVTVQGLKAGAIYVQVRAARTVAGYGRYSGMYFQMTAEAYQYSIOEKLPII 545
Db 518 IKPTNTVTVQGLKAGAIYVQVRAARTVAGYGRYSGMYFQMTAEAYQYSIOEKLPII 576
Qy 546 GSSAAGLVFLIAVVAIV-----CNRR-----GPERADSEYTDKLOH 583
Db 577 VSVTVGILLAVVIGVLLSGCCGCCGRASSLCAVAHPILIWRCGVSKAKQDPEEKMH 636
Qy 584 YTSGHM-TPQMKYIYDPTVEDPNEAVREFAKEDIDSCVKEIQVIGAGEFGEVCSHLKL 642
Db 637 FHNGHIKLPGRVTVYDPTVEDPNEAVREFAKEDIDSCVKEIQVIGAGEFGEVCSHLKL 696
Qy 643 PGKREIFVAIKLKSQYTERKORDFLSEASIMGOFDHPNVHLEGVVTKSTPVMITTEFM 702
Db 697 PGKREIFVAIKLKSQYTERKORDFLSEASIMGOFDHPNVHLEGVVTKSTPVMITTEFM 756
Qy 703 ENGLSDSLRQNDGQFTVIQLVGMGLTAAAGKYLADWNYVHRDLAARNILVNSLVCKV 762
Db 757 ENGLSDSLRQNDGQFTVIQLVGMGLTAAAGKYLADWNYVHRDLAARNILVNSLVCKV 816
Qy 763 SDFGLSRFLEDDTSDPTYSALGKIPRTAPEAIQYRKFTSASDVMSYGIVMVEVMSY 822
Db 817 SDFGLSRFLEDDTSDPTYSALGKIPRTAPEAIQYRKFTSASDVMSYGIVMVEVMSY 874
Qy 823 GERPYWDMTQDQVINAIBQDYRLPPMDCPSALHQLMDCQKORHNRKPKFQIVNTLDK 882
Db 875 GERPYWDMTQDQVINAIBQDYRLPPMDCPSALHQLMDCQKORHNRKPKFQIVNTLDK 934
Qy 883 MIRNPNSLKAMAPLSSGINLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSP 942
Db 935 LIENPSSKLTVNASCRVSNLLAEHSPGSGVSRSGFYLAFOYGGCM 994
Qy 943 DVVSQMMEDILRLGVTLACHQKILNLSQVMAQW 978
Db 995 DAVAQVTLDELRLGVTLVGHQKIMNSLOEMKVL 1030

RESULT 22
US-10-353-690-40
; Sequence 40, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacquelin
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 32427, 32427, 32427, 32427,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10332, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MP102-018P1RNNMIM
; CURRENT APPLICATION NUMBER: US/10353,690
; CURRENT FILING DATE: 2003-01-29

Prior Application Number: 60/353,224
Prior Filing Date: 2002-02-01
Prior Application Number: 60/364,529
Prior Filing Date: 2002-03-15
Prior Application Number: 60/373,861
Prior Filing Date: 2002-04-19
Prior Application Number: 60/376,287
Prior Filing Date: 2002-04-29
Prior Application Number: 60/388,080
Prior Filing Date: 2002-06-12
Prior Application Number: 60/390,971
Prior Filing Date: 2002-06-24
Prior Application Number: 60/394,130
Prior Filing Date: 2002-07-03
Prior Application Number: 60/394,797
Prior Filing Date: 2002-07-10
Prior Application Number: 60/404,904
Prior Filing Date: 2002-08-21
Prior Application Number: 60/405,450
Prior Filing Date: 2002-08-23
Remaining Prior Application data removed - See File Wrapper or PALM.
Number of Seq ID NOS: 126
Software: FastSeq for Windows Version 4.0
Seq ID NO 40
Length: 1037
Type: PRT
Organism: Homo Sapiens
US-10-353-690-40

Query Match 58.5%; Score 3036; DB 14; Length 1037;
Best Local Similarity 57.6%; Pred. No. 1.6e-191;
Matches 574; Conservative 165; Mismatches 223; Indels 34; Gaps 11;
6 LGALLLLPAAVEETLMDSTTAEGLGMVHPSPGWEVSGYDENMTTIRTVQVCNVF 65
46 LCAALRTLLSPSNEVLLDSRTWGLDGLWAFPNKWEIEGEVDENYAPIHTYQVCKVM 105
66 ESSONNWLTKFIRRRGAHRHVEMKFSVRDCSSIPVSGCKTFNLYYYEADFDSATK 125
106 EQONNWLTSWISNEGASRIFELKFTLRDCNSLPGGLGCKTFFNNYFESDDQNGR- 164
126 TFPNWMENPVKVTITIADESFQVDLGGVRMKNTEVRSFGPVSRSGFYLAQDYGGCM 185
165 ---NIKENQYIKDITIADESFTELDLGGVRMKNTEVRSFGPVSRSGFYLAQDYGGCM 221
186 SLIAVRVYRKPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245
222 ALVSVRVYKCPVSRVHLAVFPDITIGADSSQLLEVSGSCV-NHVSVDFFPWHCSAEG 280
246 EWLPIGRMCKAGFEAVENGTCRGCPSPGTFKANQDEACTHCPINSTRTTSSEATNCVC 305
281 EWLPIGRMCKAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVC 338
306 RNGYVRADLDPLDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSGGRDLVNYIICKSC 365
339 EKVFRRESDDPTWACTRPSAPRNALSNVNETSVFLEWIPPDATGGRKDVSYIACKKC 398
366 GSGRGACTRGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPQFA 425
399 NSHAGVCECGHVRVLPQSGLKNTSVMMVDDLHANTYTFEIAVNGVSDLSFGARQYV 458
426 SVNITNQAAPSIVSMHVSRTVDSITLSWQDQNGVILDIYEQYKELSEYNATA 485
459 SVNITNQAAPSIVNKKGIKAKNSISLSWQPDRENGILYIEIKHFKED-QETSYTI 517
486 IKSPNTVTVOGLKAGAIYVQVARTVAGYRGYSQWYFQMTWTEAEYQTSIOEKPLII 545
518 IKSKETITAEGLKPAVYVQIARTAGYVFSRFEFET-TPVFASSDQSLPVA 576
546 GSSNAGLVFLIAVVIAIV-----CNRR-----GFERADSYTDKLOH 583
577 VSVTVGVILLAVVIGVLLSGSCCECGGRASSLCAVAHPILIIWRGCVSKAQDPBEKMH 636

584 YTSGHM-TPGMKIYIDPPTYEDPNEAVREFAKIDISCVKIEQVIGAGERGVCSEHKL 642
Db FHNGHKLPGVRTYIDPHTYEDPNQAVHEFAKIEASCITIERVIGAGEGVCSEHKL 696
643 PGKREIFVAIKLKGSGYTEKQRDDFLSEASIMQGFQHPNVIHLEGVVTKSTPVMITEFM 702
Db PGKRELPVAIKLKGSGYTEKQRDDFLSEASIMQGFQHPNVIHLEGVVTKSTPVMITEFM 756
703 ENGLSDFLRONDQFTVIOLVGMRLGIAAGMKYLADMMYVHRDLAARNILVNSNLVCKV 762
Db ENGLSDFLRONDQFTVIOLVGMRLGIAAGMKYLADMMYVHRDLAARNILVNSNLVCKV 816
763 SDFGLSRFLDDTSDPTYSALGKPIRWTAPEATQYRKFTSASDVWSGIVMWEVMSY 822
Db SDFGLSRFLDDTSDPTYSALGKPIRWTAPEATQYRKFTSASDVWSGIVMWEVMSY 874
823 GERPYWDMTNQDVIKAVESGYRLPSPMDCPAALYQLMLDCQKERNRPFDEIVNMLDK 882
Db GERPYWDMTNQDVIKAVESGYRLPSPMDCPAALYQLMLDCQKERNRPFDEIVNMLDK 934
883 MIRNPNSLKMAPLSSGINPLDRTIPDYSNTVDLEMLAIKMGQYKESFANAGFTSF 942
Db LIRNPNSLKMAPLSSGINPLDRTIPDYSNTVDLEMLAIKMGQYKESFANAGFTSF 994
943 DVYSQMMEDILRLGVTLAGHOKKILNSIQVMRAQM 978
Db DVYSQMMEDILRLGVTLAGHOKKILNSIQVMRAQM 1030

RESULT 23
US-10-412-277-8
Sequence 8, Application US/10412277
Publication No. US20030175791A1
GENERAL INFORMATION:
APPLICANT: GUGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001067DIV
CURRENT APPLICATION NUMBER: US/10/412,277
CURRENT FILING DATE: 2003-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 975
TYPE: PRT
ORGANISM: Human
US-10-412-277-8

Query Match 58.4%; Score 3031; DB 14; Length 975;
Best Local Similarity 57.9%; Pred. No. 3.2e-191;
Matches 569; Conservative 164; Mismatches 215; Indels 34; Gaps 11;

20 EETLMDSTTATAEGLGMVHPSPGWEVSGYDENMTTIRTVQVCNVNWLTKFTIR 79
Db 3 EYNLLDSRTVMGDLGWIAPFPKNGWEEIGEVDENYAPIHTYQVCKVMEQNNWLLTSWIS 62
80 RRGARHIVEMKFSVRDCSSIPVSGCKETENLYYEADFDSATKTPNWMENPVKVD 139
Db 63 NEGASRIFELAFRTLRDCNSLPGGLGCKTFFNNYFESDDQNGR----NIKENQYIKD 118
140 TIAADESFQVDLGGVRMKNTEVRSFGPVSRSGFYLAQDYGGCMSLIARVVFYRKCP 199
Db 119 TIAADESFTELGLDGRVMKNTEVRSFGPVSRSGFYLAQDYGGCMALVSVRVYKCP 178
200 IIONGAIQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEWLVPIGRMCKAG 259
Db 179 VVRHLAVPDTITGADSSQLLEVSGSCV-NHVSVDFFPWHCSAEGWLVPIGRMCKAG 237
260 FEAVENGTCRGCPSGTFFKANQDEACTHCPINSTRTTSSEATNCVCNRYRADLDPLDM 319
Db 238 YEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCCKDYFRRESDDPTM 295

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Qy 320 PCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTRCGDNV 379
Db 296 ACTRPPSAPNAISNVNETSFWLEWIPADTGGKGVSYIAKCKNASHAGVCECGHV 355
Qy 380 QYAPRQLGLTEPRIYISDILAHTQYTEIOAVNGVTDQSPSPQFASVNIITNOAPSVA 439
Db 356 RYLPRQSLKNTVMYVDDLAHTNYTEIEBAVNGVSDLSFGARQYVSVNVTINQAESPV 415
Qy 440 SINHOVSRTVDSITLSWQDPQNGVILDYLOYYEKELSEYNATAIKSPNTNTVVOGLK 499
Db 416 TNVKKGIKANSISLSWQEDPRNGIILEYKIFKED-QETSVTIISKETITABGLK 474
Qy 500 AGAIYFQVARTVAGYGRYSGKMYFOTMTAEAYQTSIQEKLPLIGSSAAGLVFLIAV 559
Db 475 PASVYVFOIRARTAAAGYVFSRREFET-TPVFAASDQSQIPVIAVSVTVGVILLAVI 533
Qy 560 VIAIV-----CNRR-----GFERADSEYTDKLOHYTSGHM-TPGMKIY 596
Db 534 GVLLSGCCGCGGRASSLCAVAHPILIWRCGYSKAKODPEEEKHHPHNGHILPGVRTY 593
Qy 597 IDPTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLK 656
Db 594 IDPTYEDPNAVHEFAKEIEASCITIERVIGAGEFGEVCSGRLKLPKRELPVAIKTLK 653
Qy 657 SGYTEKORRDFLSPASIMGQFDHNVHLEGVVTKSTPVMIIITFMENGSLDSFLRQNDG 716
Db 654 VGYTEKORRDFLEASIMGQFDHNVHLEGVVTKSTPVMIIITFMENGSLDTPFLKNDG 713
Qy 717 QFTVIOVLVGLRGITAGMKVILADNVYHRLAARNILVNSLVCKVSDGLSRFLEDDTS 776
Db 714 QFTVIOVLVGLRGISAGMKVILSDMGYVHRLAARNILVNSLVCKVSDGLSRVLEDD-P 772
Qy 777 DPTYTSALGKIPIRWTAPALQYRKFTSADVMSYGIWVMEVMSYGERPYWDMTNDQVI 836
Db 773 EAAVTR-GGKIPIRWTAPALQYRKFTSADVMSYGIWVMEVMSYGERPYWMTNQDVI 831
Qy 837 NAIEQDYLPPMPCPSALHQLMDCWQKORNRHPRKFGQIVNTLDKMRNPNSLKAWAPL 896
Db 832 KAVEGVRPLSPMPCPAALYQLMDCWQKERNRPKFDIENVMLDKLIRNPSSLKLVNA 891
Qy 897 SSGINLPLDRTPDYTSFNTVDWLEAIKWQYKESFANAGFTSPDVUSQMMEDILRL 956
Db 892 SCRVSNLLAHSPLGSGAYSVGWLEAIKWGRYTEIFMENGYSYMDAVAQVTLLELRL 951
Qy 957 GVTLAGHOKKILNSIQVMRAQM 978
Db 952 GVTLVGHQKKIMNSLOEMKVQL 973
```

RESULT 24

```
US-09-823-187-40
; Sequence 40, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taudier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
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; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-187-40

Query Match 58.4%; Score 3028; DB 10; Length 998;
Best Local Similarity 59.1%; Pred. No. 5.2e-191;
Matches 574; Conservative 153; Mismatches 224; Indels 20; Gaps 9;

Qy 17 AAVEETLMDSTTAAELGMMVHPSPGWEVSGYDENMNTIRTYQVCNVFSSONNWLRTK 76
Db 29 AAKEVLLDLSKAQOTLEWISSPPNGWEEISGLDENYTPRTYQVCVMPNQNWLRTN 88
Qy 77 FIRRGARHRIHVEMKFSVRDCSSIPSVPGSKETFNLYYEADPDSATKTFPNMNPV 136
Db 89 WISGNAQRIFVELKFTLRDCNSLPGVLGTCETFNLYYETDYE----TGRNIRENLV 144
Qy 137 KVDTIAADESFSQVDLCGRVKNINTEVRSPGVSRSRGFYLAQDYGCSCMLIAVRYR 196
Db 145 KIDTIAADESFTQDGLGERKMKLNTREVRIGPLSKKGFYLAQDVGACIALVSVKVY 204
Qy 197 CPRIIONGALFQBTLSGAESTSLVAARGSCIANA-BEVDVPIKLYCNGDGEWLVPIC 255
Db 205 CWSIIENALFPDVTVGSEFSSVLVVRGTCSSABEEAENAPRMHCSABEWLVPIK 264
Qy 256 CKAGFEAVENGTVCRGCPSTFKANQOGEACTHCIPINSRTTSEGATNCVCNRYRAD 315
Db 265 CKAGYQ--QKGDTCPCGRCGRFYKSSQDLQCSRCPHSPDSKSSRCECEDGYRAPS 322
Qy 316 PLDMPCCTTPSAQAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACT 375
Db 323 PYYVACTRPPSAPQNLIFNINQTTVSLWSPPADNGGRNDVTYRILCKRCSWEQEC 382
Qy 376 GDNVQYAPRQLGLTEPRIYISDILAHTQYTEIOAVNGVTDQSPSPQFASVNIIT 435
Db 383 GSNIGNPQOTGLENDNYVTMDLLAHANYTFEVAENVGSDLSRSQRLFAVSLTTQ 442
Qy 436 PSASIMHQSRTVDSITLSWQDPQNGVILDYLOYYEKELSEYNATAIKSPNTNTV 495
Db 443 PSQVSGWKERVQLQRSVELSWQEPHNGVITEYIKYEKQDRERTYSTVTKTSTASI 502
Qy 496 QGLKAGAIYFQVARTVAGYGRYSGKMYFOTMTAE-----EYQTSIQEKLPLIG 548
Db 503 NNLKPGTVYVFOIRARTAAAGYVFSRREFET-TPVFAASDQSQIPVIAVSVTV 562
Qy 549 AAGLVFLIAVAVVIAVCNRR-GFERADSEYTDKLOHYTSGHMTPGMKIYIDPFT 607
Db 563 VAGTIIILVFMVFGFIIGRRHCGYSKADQEGDESLYFH---FKPGTYTIDPTEY 619
Qy 608 AVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEK 667
Db 620 AVHQFAKELDASCKIERVIGAGEFGEVCSGRLKLPKRDVAVAIKTLKVGYTEK 679
Qy 668 LSEASIMGQFDHNVHLEGVVTKSTPVMIIITFMENGSLDSFLRQNDGQFTVIO 727
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Db 680 LCEASIMGQFDHPNVHLEGVVTRGKPMVIVIEFMENGALDAFLRKHGQFTVQLVGM 739
QY 728 RGIAAGMKYLDADNYYVHRLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGK 787
Db 740 RGIAAGRYLDADNYYVHRLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGK 797
QY 788 IPIRWTAPEAIQYRKFTSADSVMSYGVIMVWVMSYGERPYMDTNDQVINAIEQDYRLPP 847
Db 798 IPIRWTAPEAIQYRKFTSADSVMSYGVIMVWVMSYGERPYMDTNDQVINAIEQDYRLPP 857
QY 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMINRPNLSLKAWAPLSSGINLPLDR 907
Db 858 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMINRPNLSLKAWAPLSSGINLPLDR 917
QY 908 TTPDVTSTFNTVDLEIAIKMGQYKESFANAGFTSFVVVSQMMEDILRLGLVTLACHOKKI 967
Db 918 TTPDVTSTFNTVDLEIAIKMGQYKESFANAGFTSFVVVSQMMEDILRLGLVTLACHOKKI 977
QY 968 LNSIQVMRAQM 978
Db 978 MSSIQTMRAQM 988

RESULT 25

US-09-823-187-42
; Sequence 42, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-823-187-42

Query Match 58.1%; Score 3013; DB 10; Length 998;
Best Local Similarity 58.6%; Pred. No. 5.1e-190;
Matches 572; Conservative 157; Mismatches 217; Indels 30; Gaps 11;

QY 17 AAVETLMDSTTAAELGVMVHPPSGHVEVSGVDENNNTIRTYQVCNVFESSQNNWLRTK 76
Db 29 AAKEVLLDSKAQOTELWISPPSGWEEISGLDENYTPRTYQVCNVFESSQNNWLRTN 88
QY 77 FIRRGAAHRIHVMKESVRDCSSITPSVPGCKETENLYYEADFDSDATKTFPNMNPWV 136
Db 89 WISKGNARLIFVELKFTLRDCNSLPGVLGCKETENLYYETDYD---TGRNIRENLYV 144
QY 137 KVDITAADESFSQVDLGGVRVMKINTEVRSFPGVSRSGFYLAFOYDGGCMLIAVRVYFRK 196
Db 145 KIDITAADESFTQDLGERKMKLNTVEIREIGPLSKGFLYAFODVGACIALVSKVYKK 204
QY 197 CPRII QWCAI FOETLSAESTSLVAARGSCIANA--EEVDVPIKLYCNGDGEWLVPTGRCM 255
Db 205 CWTIVENLAVFPDITVTSSEFSLVEVRGTCSVAEEAEENSPRMHCSAGEWLVPTGKCI 264
QY 256 CKAGFAVENGTVCRCGPGTFFKANOGDEACTHCIPINSRTTSGATNCVCNRYGYRADLD 315
Db 265 CKAGYQ--QKGDTCPCGRRFYKSSQDLQCSRCPHSPDSRSGRCEDEGYIRAPSD 322
QY 316 PLDMPCTTTPSAPQAVISSVNETSLMELWTPPRDSCGREDLVNII CKSGSGRGACTRC 375
Db 323 PPIVACTRTPSPAPQNLIFNINQTTVSLWSPADNGGRNDVTYRILCKRCSWEOGECVPC 382
QY 376 GDNVQVAPROLGLTEPRIVISDLAHTQYTERIQAVNGVTDQSPSPQFASNITTNOAA 435
Db 383 GSNIGVWPOOTGLNEDNYIVMDLAAHANTFEVEAVNGVSDLSRSORLFAAVSITIGQAA 442
QY 436 PSAVIMHQVSRVTSITLSWSQPDOPNGVILDYELQYKELSEYNATAIKSPNTVTIV 495
Db 443 PSQVSGVMKERVLRQSVQLSWQEPHPNGVITEYEIKYKQQRERTYTLTKTSASIS 502
QY 496 OGLKAGAIYVQVRARTVAGYGRYKMYFQNTWEA-----EYQTSIQEKLPLIGS--S 548
Db 503 NNLKPGTVYVQIRAVTAAGYGNYSPLDVATLEASGRMFEATAVSSSQNPVIIAVVA 562
QY 549 AAGLFLIAVWIAI VCNRR--GFERADSBYTDKLOHYTSHMTPGMKIYIDPFTVEDPNE 607
Db 563 VAGTILVFMVFGFIIGRHCYKADQSGDELFH---FKFPGTKYIDPFTVEDPNE 619
QY 608 AVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDF 667
Db 620 AVHQFAKELDASCIEKIERVIGAGEFGEVCSGRLKLPQGRDVAIVAKTLKVGYTEKQRDF 679
QY 668 LSEASIMGQFDHPNVHLEGVVTRKPMVITEFMENGSLDSFLQNDGQFTVQLVGM 727
Db 680 LCEASIMGQFDHPNVHLEGVVTRKPMVITEFMENGSLDSFLQNDGQFTVQLVGM 739
QY 728 RGIAAGMKYLDADNYYVHRLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGK 787
Db 740 RGIAAGRYLDADNYYVHRLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGK 797
QY 788 IPIRWTAPEAIQYRKFTSADSVMSYGVIMVWVMSYGERPYMDTNDQVINAIEQDYRLPP 847
Db 798 IPIRWTAPEAIQYRKFTSADSVMSYGVIMVWVMSYGERPYMDTNDQVINAIEQDYRLPP 857
QY 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMINRPNLSLKAWAPLSSGINL 902
Db 858 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMINRPNLSLKAWAPLSSGINL 912
QY 903 PLLDRTIPDYSFNTVDLEIAIKMGQYKESFANAGFTSFVVVSQMMEDILRLGLVTL 962
Db 913 PLLDQSTPDTAFPCSVGEWLOAKMERYKDNFTAGYNSLESVARMTIDDDVMSLGITLVG 972
QY 963 HOKKILNSIQVMRAQM 978
Db 973 HOKKIMSSIQTMRAQM 988

RESULT 26
US-09-823-187-43
; Sequence 43, Application US/09823187


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Db      29 EVNLLDSKTIQBELGWSYPSHGWEISGVDEHYTPRTYQVCNVMDSHSONNWLNTNVP 88
Qy      80 RRGARHIVHEMKSVPDCSSIPVPSCKETNLYYYEADFSAKTTPNMNMENPWKVD 139
Db      89 RNSAQKIYVELKFTLRDCNSIPLVLGTCKETNLYYMSDDDHGVK----FREHQTAKID 144
Qy     140 TIAADESFQVDLGGRWKINTEVRSFGVPSRSGFYLAPODYGGCWSLIAVRVFKCPR 199
Db     145 TIAADESFQMDLGRILKLNTEIREVGVNKGKGYLAPODVGCACVALSVRVYFKCPCF 204
Qy     200 ITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPTIGRCMKAG 259
Db     205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLPIGKSCNAG 262
Qy     260 FEAVENGTVCRCPGCTFKANQDEACTHCPINSRTTSEGATNCVCRNGYVRADLDPLDM 319
Db     263 YE--ERGFMCQACRPGFYKALDGNMKCAKCPHSSSTQEDGSMNCCENNYFRADKPPSM 320
Qy     320 PCTTIPSAQVAIVSSVNETSLMLEWTPPRDSGREDLVNIIKSCSGRGACTRCGDNV 379
Db     321 ACTRPPSSPRNVISINETSVIDLWSWPLDTGGRKDVTFNIIKCKGWNIIKQCEPCSPNV 380
Qy     380 QYAPRLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPOPASVNIITNOAAPS 439
Db     381 RELPRQFGLTNTVTVDLLAHTNTYFEIDAVNGVSELSPPRQFAAVSIITNOAAPS 440
Qy     440 SIMHQVSRVDSITLSWSQOPQNGVILDYLOYYEKELSEYNATAIKSPNTVTVOGLK 499
Db     441 LTIKDRTSRNSISLSWQEPHPNGIILDYEVKYEKQEQSTYTLRAGTNTVTSLSK 500
Qy     500 AGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSAAGLVFLI 559
Db     501 PDTIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSAAGLVFLI 559
Qy     560 VIAYV---CNRGPERADSEYTKLQHYTSGHM--TPGKMIYIDPFTVEDNEAVREPAKE 615
Db     560 IYVLIGRCFGYKXGAD----EKKLHFGNHLKLPGLRTYVDHTYEDPTQAVHEPAKE 615
Qy     616 IDISCVKIBOVIGAGEPGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRFLSEASIM 675
Db     616 LDATNISDKVVGAGEPGEVCSGRLKLPKSKKEISVAIKTLKVGYTEKQRDRFLGEASIM 675
Qy     676 QFDHNVHLRGVTKSPVMIITFPMENGLDSEFLQNDQOFTVIOLVGMRLGIAAGMK 735
Db     676 QFDHNPRIIRLEGVVTKSPVMIITFPMENGLDSEFLKRDQAQFTVIOLVGMRLGIAAGMK 735
Qy     736 YLADNMYVHRDLAARNILVNSNLVKYSDFLSFLFLEDDTSDPTTYSALGKPIRTWAP 795
Db     736 YLSDMGVYHRDLAARNILVNSNLVKYSDFLSFLFLEDD--PEAYITR--GKPIRTWSP 793
Qy     796 EAIQYRKFTSASDVMSYGIVMWEVMSYGERPYWDMTNDQVINAEQDYRLPPPMDCPSAL 855
Db     794 EAIYRKFTSASDVMSYGIVMWEVMSYGERPYWEMSNDQVIKAVDEGYRLPPPMDCPSAL 853
Qy     856 HOLMDCQKDRNRHPRFGQIWNLTDKMIRNPNSLKAWPLSSGINLPLIDRTIPDYSF 915
Db     854 YQLMDCQKDRNRHPRFQIWSLIDKLIIRNPGSLKIITSAARPNSLLDQSNVDISTF 913
Qy     916 NTVDEWLEAIKMGOKYESFANAGFTSPDVVSQMMEDILRLGVLTAHQKILNISTQVMR 975
Db     914 RTTGWLNGVTRACHCKBIFTGVEYSSCDTIATKSTDDMKKGVTVVGPQKKIISIKALE 973
Qy     976 AQ 977
Db     974 TQ 975
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RESULT 28

US-10-205-823-97

; Sequence 97, Application US/10205823

; Publication No. US20030108963A1

; GENERAL INFORMATION:

```
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kanatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-97
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Query Match 56.5%; Score 2930.5; DB 14; Length 983;

Best Local Similarity 57.0%; Pred. No. 1.4e-184;

Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

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Qy      20 EETLMDSTTATLGMVHPSPSGWEVSGYDENMTIARTYQVCNVPFESSONNWLTKIR 79
Db      29 EVNLLDSKTIQBELGWSYPSHGWEISGVDEHYTPRTYQVCNVMDSHSONNWLNTNVP 88
Qy      80 RRGARHIVHEMKSVPDCSSIPVPSCKETNLYYYEADFSAKTTPNMNMENPWKVD 139
Db      89 RNSAQKIYVELKFTLRDCNSIPLVLGTCKETNLYYMSDDDHGVK----FREHQTAKID 144
Qy     140 TIAADESFQVDLGGRWKINTEVRSFGVPSRSGFYLAPODYGGCWSLIAVRVFKCPR 199
Db     145 TIAADESFQMDLGRILKLNTEIREVGVNKGKGYLAPODVGCACVALSVRVYFKCPCF 204
Qy     200 ITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPTIGRCMKAG 259
Db     205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLPIGKSCNAG 262
Qy     260 FEAVENGTVCRCPGCTFKANQDEACTHCPINSRTTSEGATNCVCRNGYVRADLDPLDM 319
Db     263 YE--ERGFMCQACRPGFYKALDGNMKCAKCPHSSSTQEDGSMNCCENNYFRADKPPSM 320
Qy     320 PCTTIPSAQVAIVSSVNETSLMLEWTPPRDSGREDLVNIIKSCSGRGACTRCGDNV 379
Db     321 ACTRPPSSPRNVISINETSVIDLWSWPLDTGGRKDVTFNIIKCKGWNIIKQCEPCSPNV 380
Qy     380 QYAPRLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPOPASVNIITNOAAPS 439
Db     381 RELPRQFGLTNTVTVDLLAHTNTYFEIDAVNGVSELSPPRQFAAVSIITNOAAPS 440
Qy     440 SIMHQVSRVDSITLSWSQOPQNGVILDYLOYYEKELSEYNATAIKSPNTVTVOGLK 499
Db     441 LTIKDRTSRNSISLSWQEPHPNGIILDYEVKYEKQEQSTYTLRAGTNTVTSLSK 500
Qy     500 AGAIYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSAAGLVFLI 559
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Db 501 PDIYVQIARATAGTNSRKPEFETSPDS- FSISSGSSQVVMIAISAVALITTV 559
Qy 560 VIAIV---CNRRGPERADSEYTKLOHYTSGHM-TPGMKIYIDPFTYEDPNEAVREFAKE 615
Db 560 IYVLIGRFGCGYKSKHGAD---EKRLHFGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKE 615
Qy 616 IDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRFLSEASIMG 675
Db 616 LDATNISIDKVGAGEFGEVCSGRLKLPKSKKEISVAIKTLKVGYTEKQRDRFLSEASIMG 675
Qy 676 QFDHPNVIHLEGVVTKSTPWMIITEPMENGSLDSFLRQNDGQFTVIOVLGMLGIAAGMK 735
Db 676 QFDHPNIIIRLEGVVTKSKPMIVTEPMENGSLDSFLRKHDAQFTVIOVLGMLGIAAGMK 735
Qy 736 YLADNMVYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGKPIRWTPAP 795
Db 736 YLSDMGVYVHRDLAARNILVNSLVCKVDFGLSRVLEDD-PEAAYTTR-GGKPIRWTPSP 793
Qy 796 EAIQYRKFTSASDWSYGIWMEVMSYGERPYDMTQNDVINAIEQDYRLPPMDCPSAL 855
Db 794 EAIAYRKFTSASDWSYGIWMEVMSYGERPYEMSNQDVIKAVDEGYRLPPMDCPSAL 853
Qy 856 HOLMLDCWQDRNHRPKFGQIVNTLDKMIKRNPSLKAAPLSSGINPLDRTIPDYTSF 915
Db 854 YQLMLDCWQDRNHRPKFQIVSILDKLIRNPSGLKIITSAARPSNLLDQSNVDISTF 913
Qy 916 NTVDWLEAIKMGQYKESFANAGFTSPDVVSQMMEDIILRGVTLAGHKILNSIQVMR 975
Db 914 RTTGDWLVNGVYTAHCKEIFTGVEYSSCDTAKISTDDMKKVGVTVGPKKIISIKALE 973
Qy 976 AQ 977
Db 974 TQ 975

RESULT 29
US-10-345-680-2
; Sequence 2, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sinos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323.
; TITLE OF INVENTION: 12303, 985, 12237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: ME102-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
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; ORGANISM: Homo Sapiens
US-10-345-680-2
Query Match 56.5%; Score 2930.5; DB 14; Length 983;
Best Local Similarity 57.0%; Pred. No. 1.4e-184;
Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

Qy 20 EETLMDSTTATABELGMVHPSPSCWEEVSGYDENMTIRTYQVCNVFESSQNNLRTKPIR 79
Db 29 EVNLLDSKTIQELGELMISYPSHGWEISGVDEHYTPIRTYQVCNVMDHSQNNLRTNWVP 88
Qy 80 RRGARHIVHEMKSVSDCSSIPSPGSKETFNLYYYEADFDSATKTFFPWMMENPWTKVD 139
Db 89 RNSAQKIYVELKFTLDCNSIPLVLTGCKETFNLYYMESDDDHGVK----FHEHQFTKID 144
Qy 140 TIAADSFSDVLDGGRVMKINTEVRSGFVPSRSGFLAFODYGGCNSLIARVVFYRKCPR 199
Db 145 TIAADSFSTQMDLQDRILKLNTEIREVGNPKGFLAFQDVGACVALSVRYVFKCPCF 204
Qy 200 IIQNGAIFQBTLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRMCCKAG 259
Db 205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLVPIGKCSNAG 262
Qy 260 FEAVENGTVCRGCPSTGTFKANQDEACTHCPINSRTTSEGATNCVCGYGYRADLPLDM 319
Db 263 YE--ERGFMCQACRPGFYKALDGNMKCAKCPHSHSTQEDGSMNCRCENNYFRADKDPSP 320
Qy 320 PCTTIPSAQAVTSVSVNETSLMLEWTPPRDSGREDLVNIIICKSCSGRGACTTRCGDNV 379
Db 321 ACTRPSSPRNVLSNINETSIVLDWSWPLDTGKGVTFNIIICKCGWNIIKQCEPCSPNV 380
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTITNQAPSAV 439
Db 381 RFLPRQFGLTNTVTVDLLAHTNYTFEIDAVNGVSELSPPRQFAAVSITTNQAPSPV 440
Qy 440 SIMHVSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSTNTVTVOGLK 499
Db 441 LTIKDORTSRNSISLSWQEPHNGIILDEYEVYKEQEQTSTYTLRABGTNVTISLK 500
Qy 500 AGAIYVQVRAITVAGYRGYSGWYFOTMTEAEVQTSIOEKLPLIIGSSAAGLVFLAVV 559
Db 501 PDIYVQIARATAGTNSRKPEFETSPDS- FSISSGSSQVVMIAISAVALITTV 559
Qy 560 VIAIV---CNRRGPERADSEYTKLOHYTSGHM-TPGMKIYIDPFTYEDPNEAVREFAKE 615
Db 560 IYVLIGRFGCGYKSKHGAD---EKRLHFGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKE 615
Qy 616 IDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRFLSEASIMG 675
Db 616 LDATNISIDKVGAGEFGEVCSGRLKLPKSKKEISVAIKTLKVGYTEKQRDRFLSEASIMG 675
Qy 676 QFDHPNVIHLEGVVTKSTPWMIITEPMENGSLDSFLRQNDGQFTVIOVLGMLGIAAGMK 735
Db 676 QFDHPNIIIRLEGVVTKSKPMIVTEPMENGSLDSFLRKHDAQFTVIOVLGMLGIAAGMK 735
Qy 736 YLADNMVYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGKPIRWTPAP 795
Db 736 YLSDMGVYVHRDLAARNILVNSLVCKVDFGLSRVLEDD-PEAAYTTR-GGKPIRWTPSP 793
Qy 796 EAIQYRKFTSASDWSYGIWMEVMSYGERPYDMTQNDVINAIEQDYRLPPMDCPSAL 855
Db 794 EAIAYRKFTSASDWSYGIWMEVMSYGERPYEMSNQDVIKAVDEGYRLPPMDCPSAL 853
Qy 856 HOLMLDCWQDRNHRPKFGQIVNTLDKMIKRNPSLKAAPLSSGINPLDRTIPDYTSF 915
Db 854 YQLMLDCWQDRNHRPKFQIVSILDKLIRNPSGLKIITSAARPSNLLDQSNVDISTF 913
Qy 916 NTVDWLEAIKMGQYKESFANAGFTSPDVVSQMMEDIILRGVTLAGHKILNSIQVMR 975
Db 914 RTTGDWLVNGVYTAHCKEIFTGVEYSSCDTAKISTDDMKKVGVTVGPKKIISIKALE 973
Qy 976 AQ 977
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Db 974 TQ 975
RESULT 30
US-10-295-027-602
; Sequence 602, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 016501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 602
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-602

Query Match 56.5%; Score 2930.5; DB 14; Length 983;
Best Local Similarity 57.0%; Pred. No. 1.4e-184;
Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

Qy 20 EETLMDSTTAAELGVMVHPSPGVEEYSGVDENMNTIRTYQVCNVFSSQNNMLRTKFR 79
Db 29 EVNLLDSKTIGELGWSYPSHGWEESGVDEHYPTIRTYQVCNVMDHSQNNMLRTNWVP 88
Qy 80 RRGARHIVEMKFSVRDCSSIPSPVSGSKETFNLYYYEADFSDATKTFPNMNPWKVD 139
Db 89 RNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDHGK----FREHQTKID 144
Qy 140 TIAADESFQVDLGRVYMKINTEVRSFQVSRSGFYLAFOYDYGCMSLIAVRVYFKCPR 199
Db 145 TIAADESFQMDLGRILKUNTEIREVGNPKGFLAFQDVGACVALSVRVYFKCPR 204
Qy 200 IIONGALFOETLSGAESTSLVAARGSCITANAEVVDVPIKLYCNGDGEWLVPIGRCMCKAG 259
Db 205 TVKULAMFPDTPV-MDSQSLVEVRGSCVNNKEDPP-RMYCSTEGEWLVPIGKCSNAG 262
Qy 260 FEAVENGTVCRGCPGSGFTFKANQDGEACTHCPINRSITSEGATNCVCRNGYRADLDPLDM 319
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Job time : 166 secs